

## TEG1

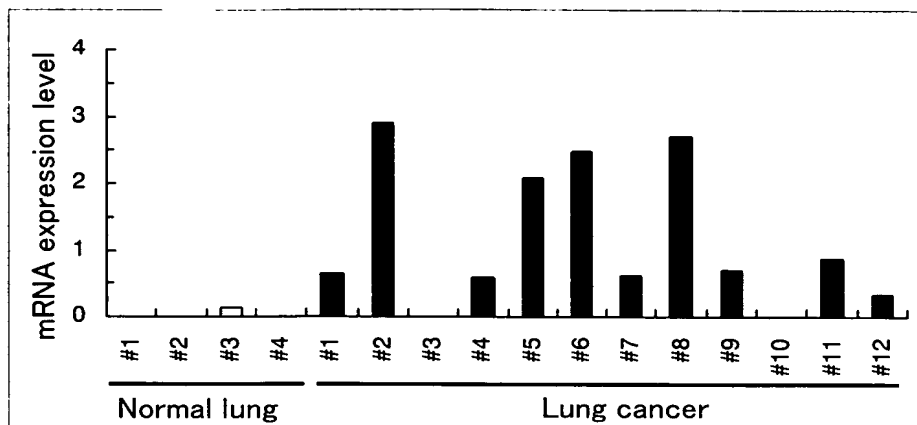


FIG.1

## TEG2(Large bowel cancer )

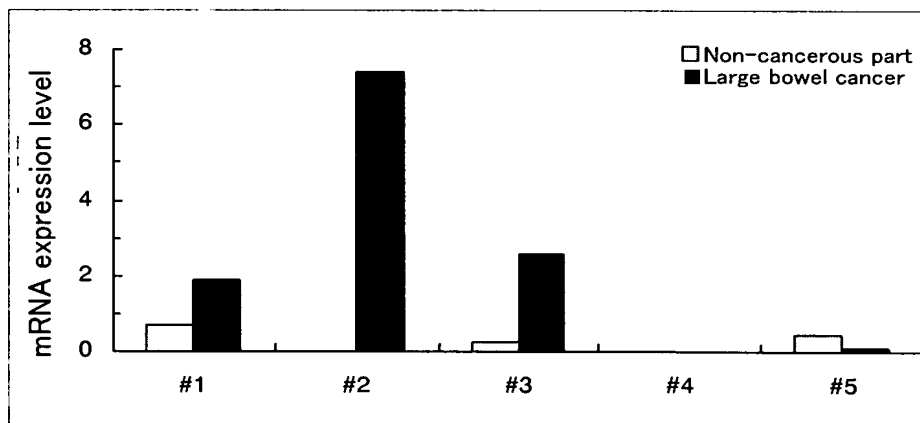


FIG. 2

TEG2 (Stomach cancer )

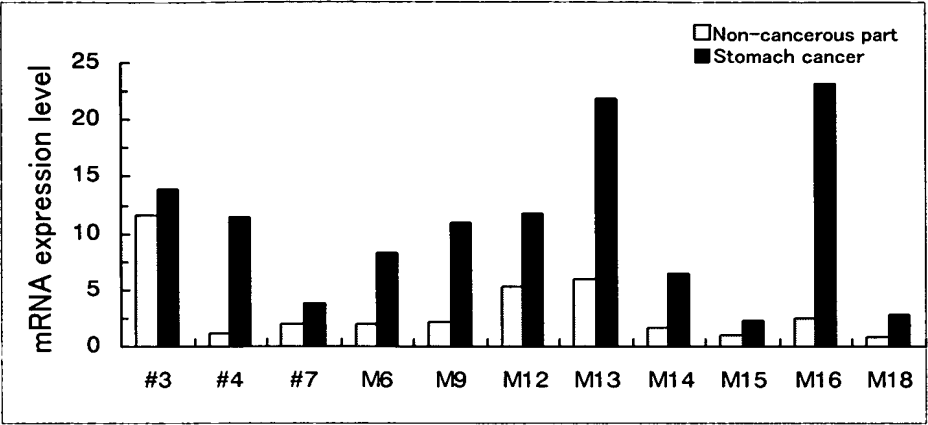


FIG. 3

TEG3

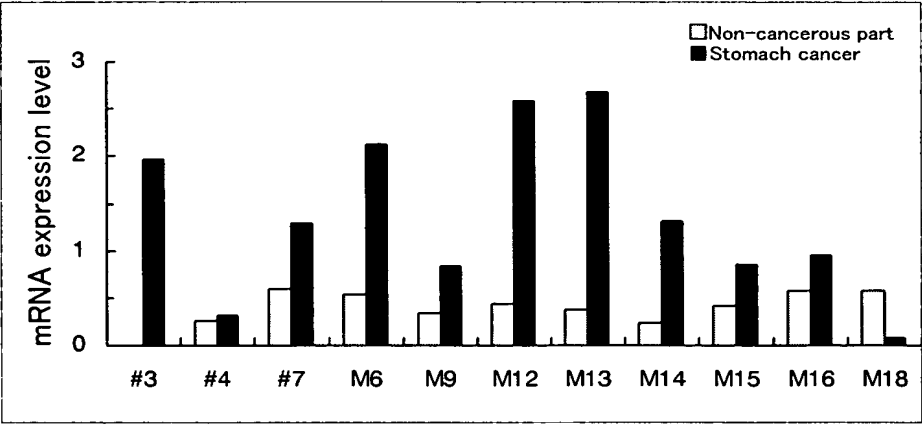


FIG. 4

## TEG4

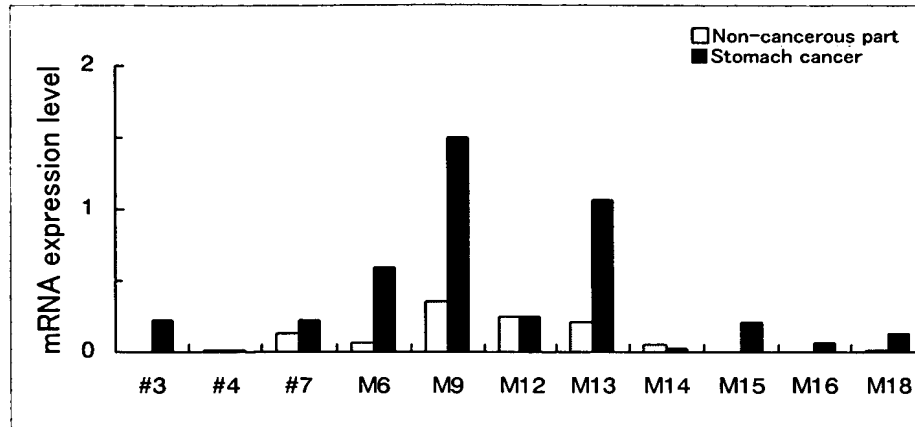


FIG. 5

## TEG5

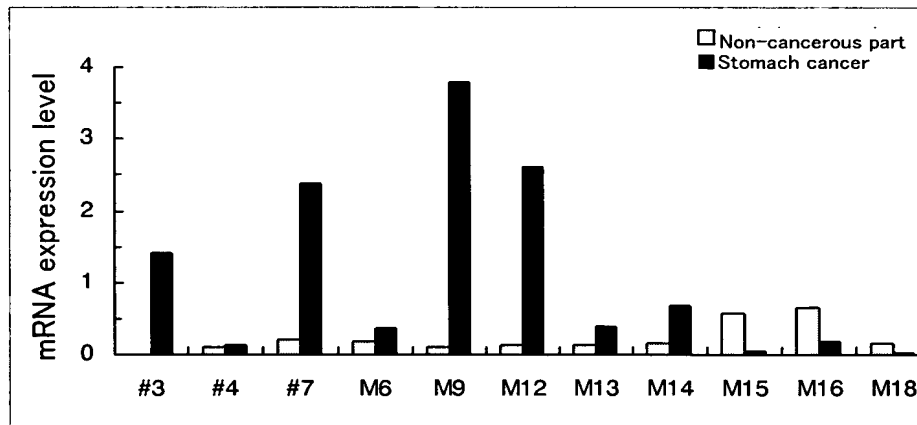


FIG. 6

## TEG6(Large bowel cancer )

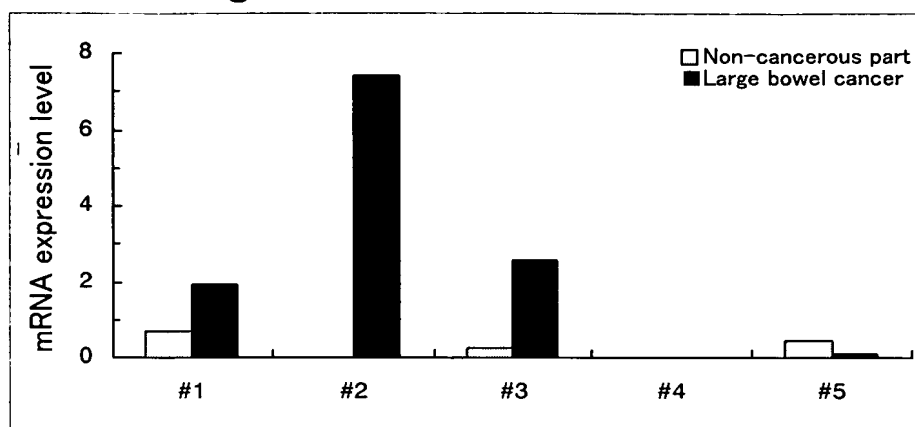


FIG. 7

## TEG6(Stomach cancer )

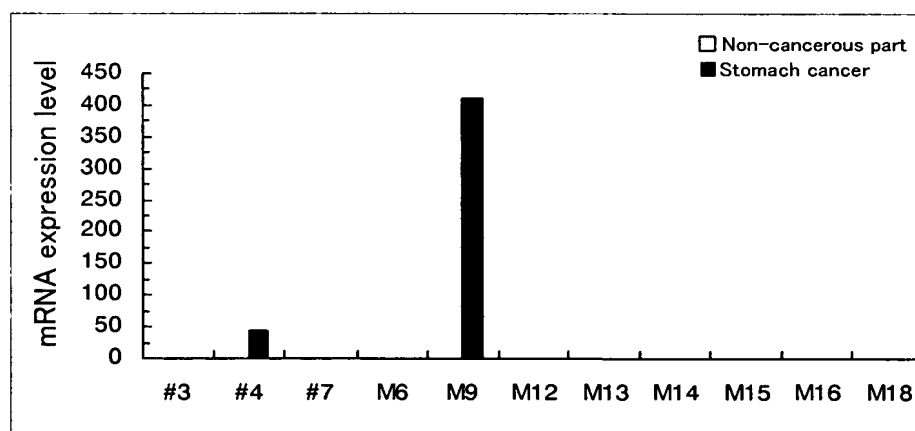


FIG. 8

## TEG7

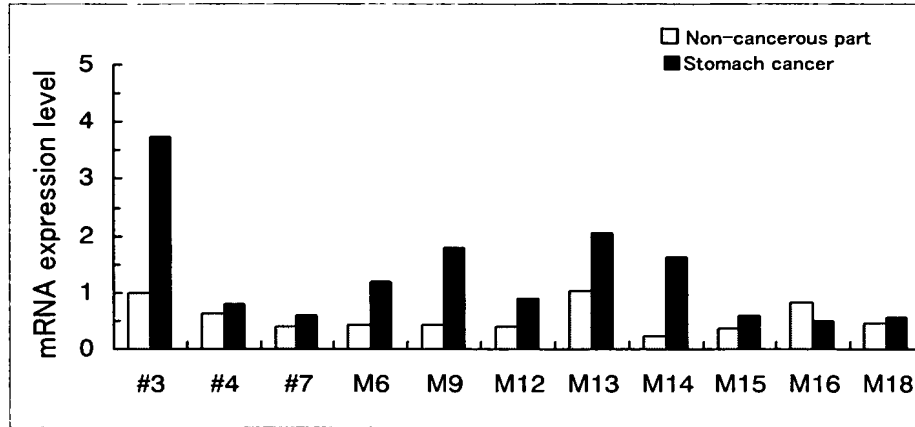


FIG. 9

## TEG8

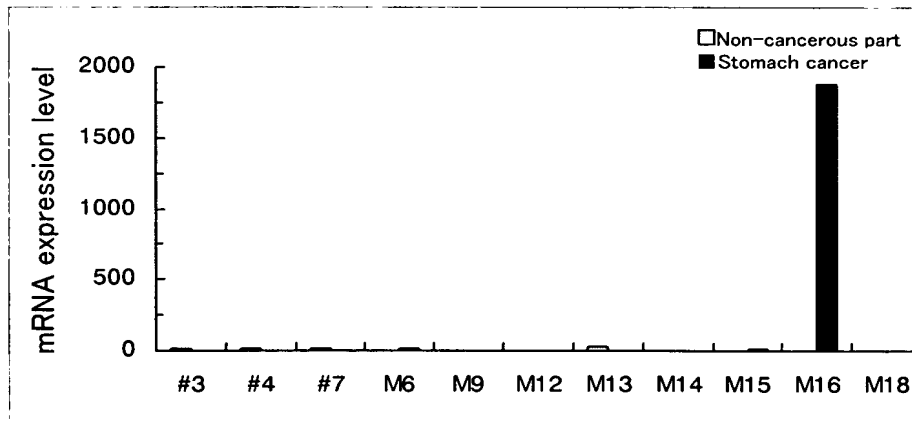


FIG. 10

## TEG9

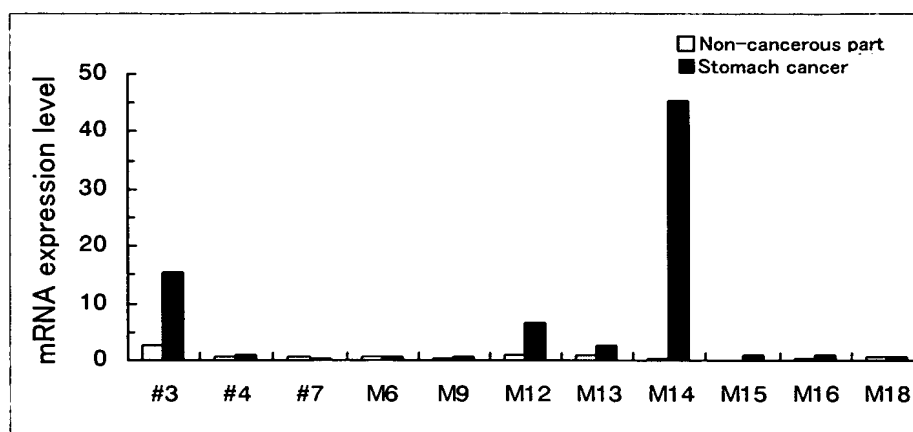


FIG. 11

## TEG10

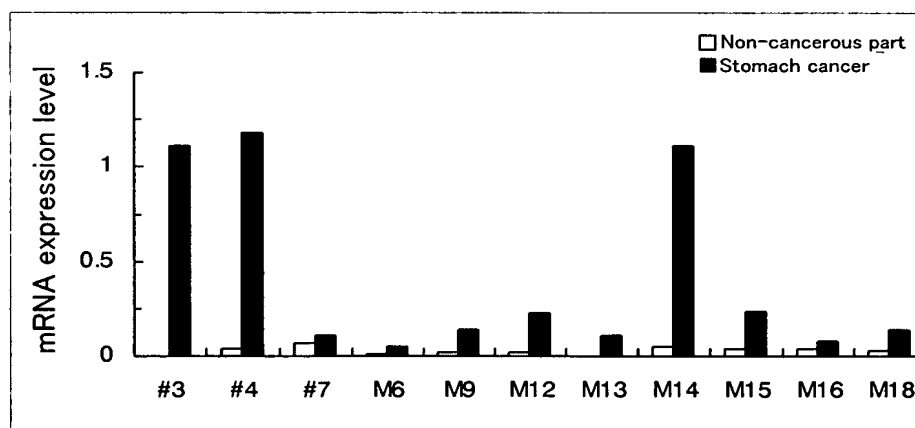


FIG.12

## TEG11

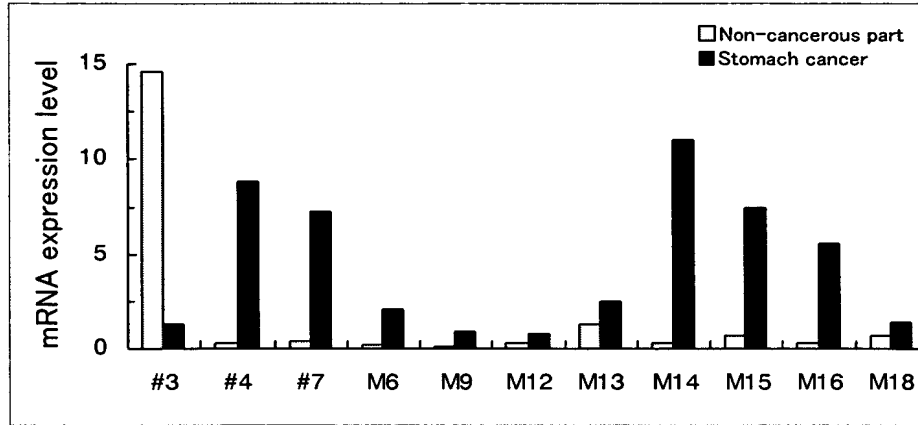


FIG. 13

## TEG12

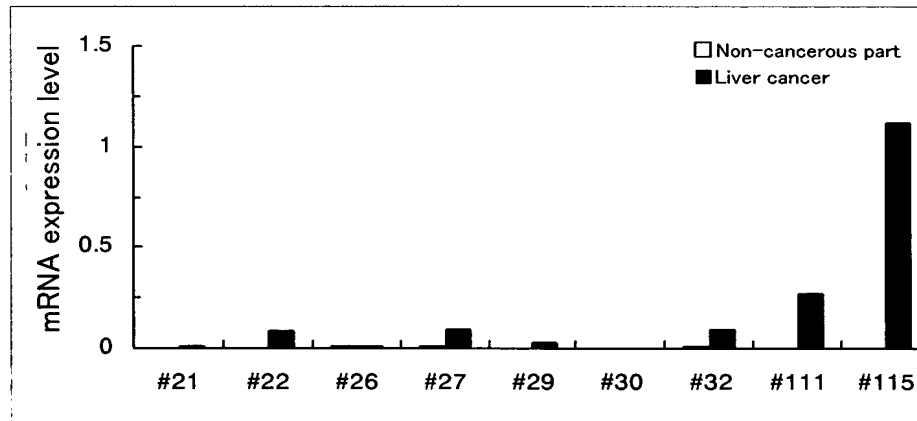


FIG. 14

## TEG13

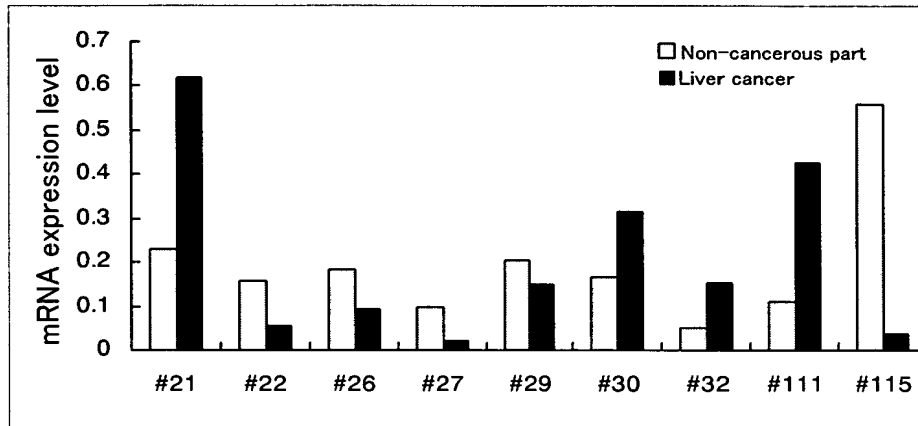


FIG. 15

## TEG14

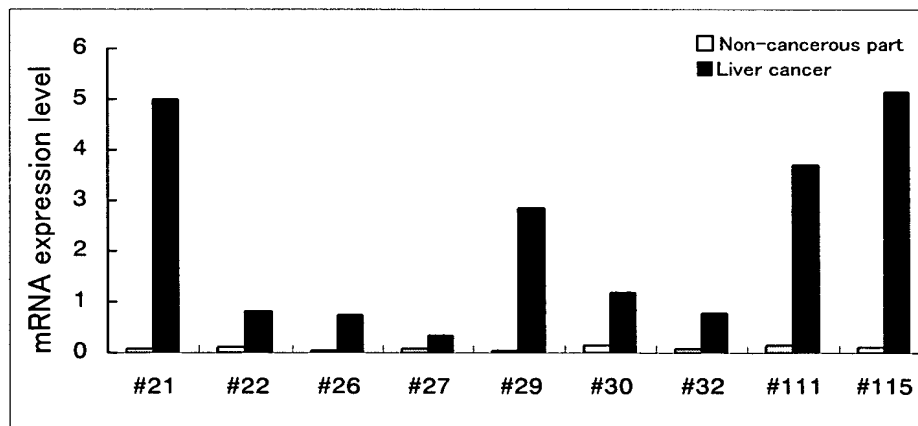


FIG. 16



## TEG15

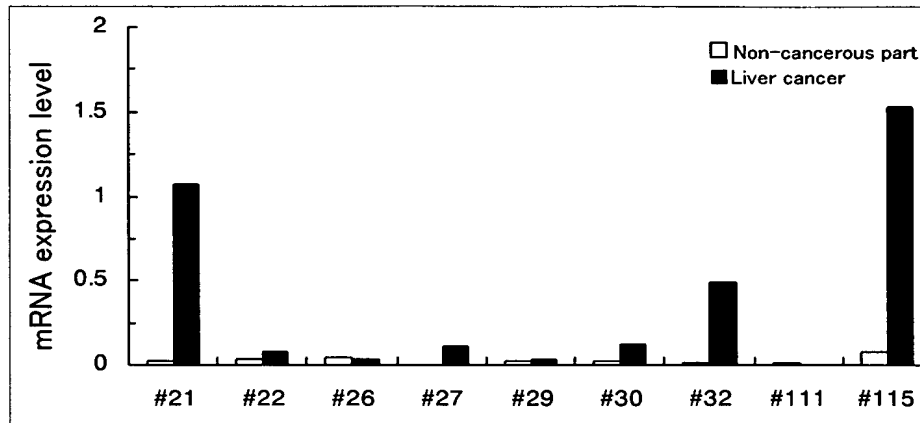


FIG. 17

## TEG16

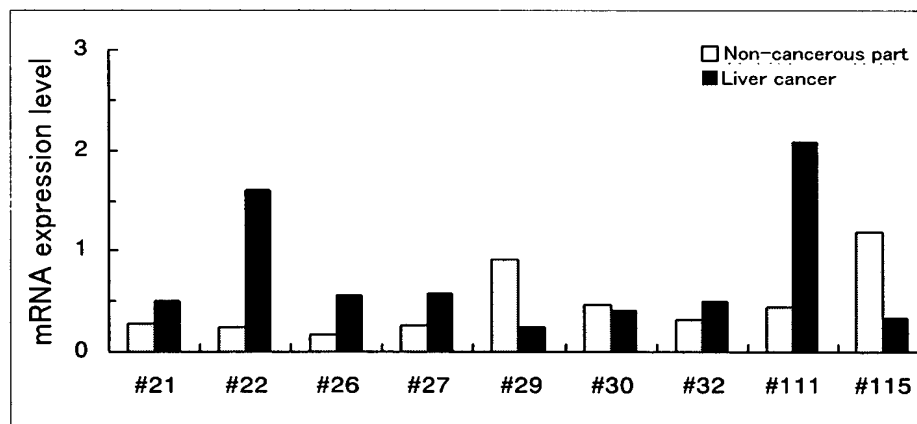


FIG. 18

## TEG17

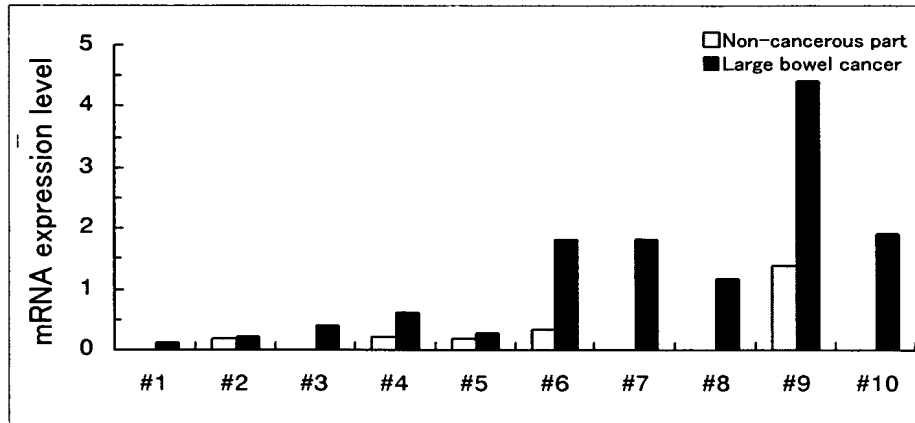


FIG. 19

## TEG18

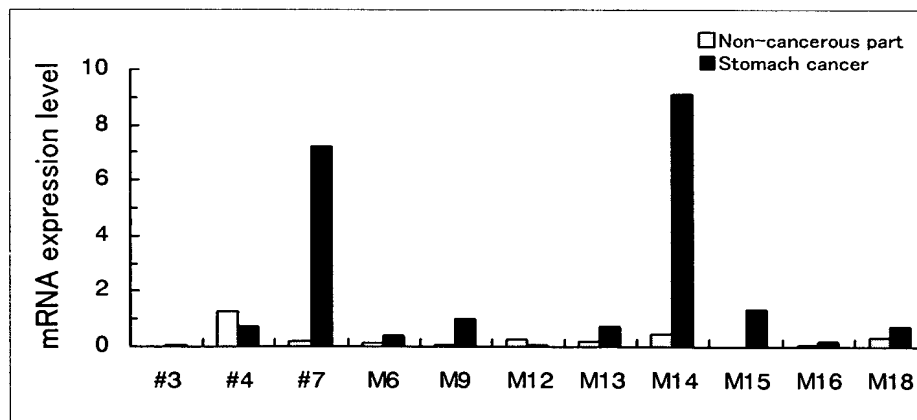


FIG. 20

## TEG19

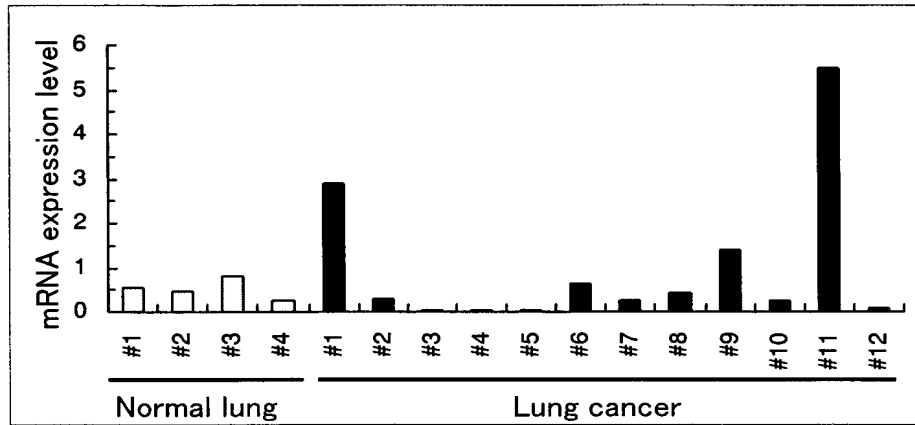


FIG. 21

## TEG20

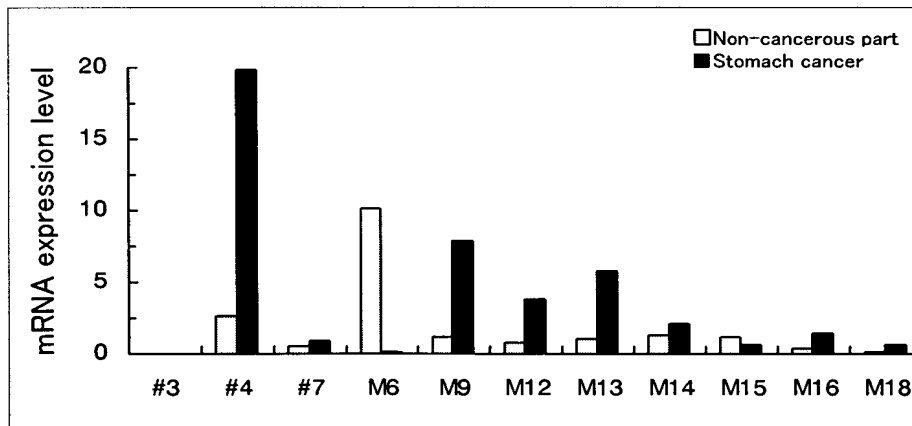


FIG. 22

## TEG21

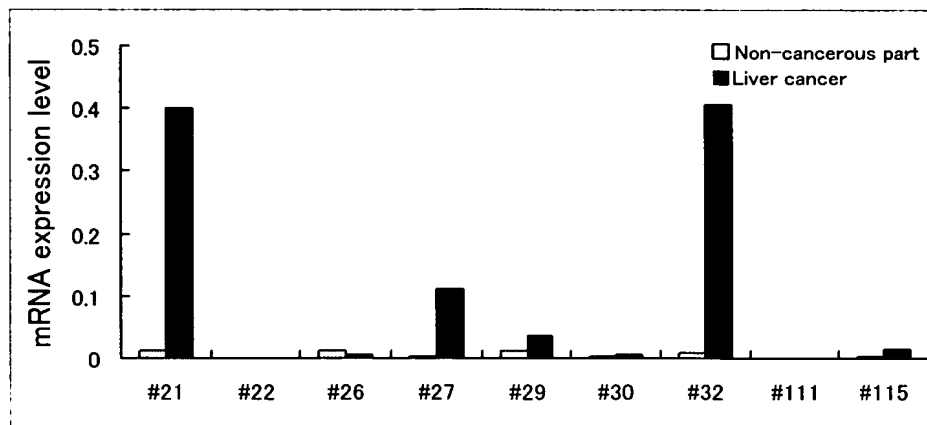


FIG. 23

## TEG22

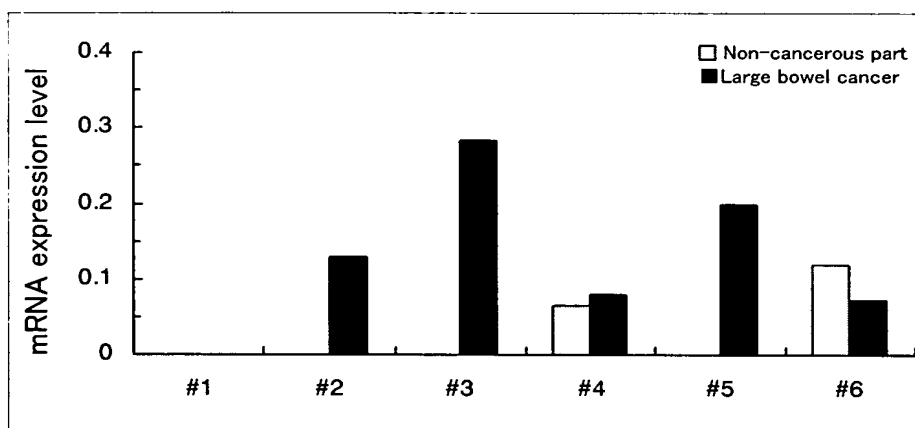


FIG. 24

13/66

## TEG23

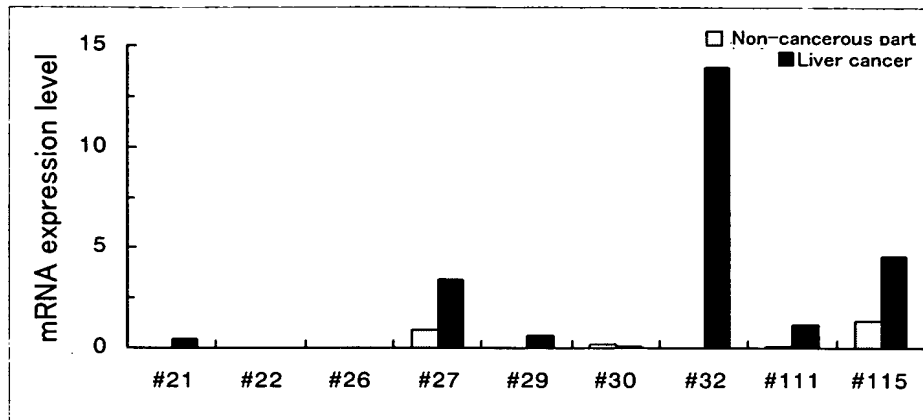


FIG. 25

## TEG24

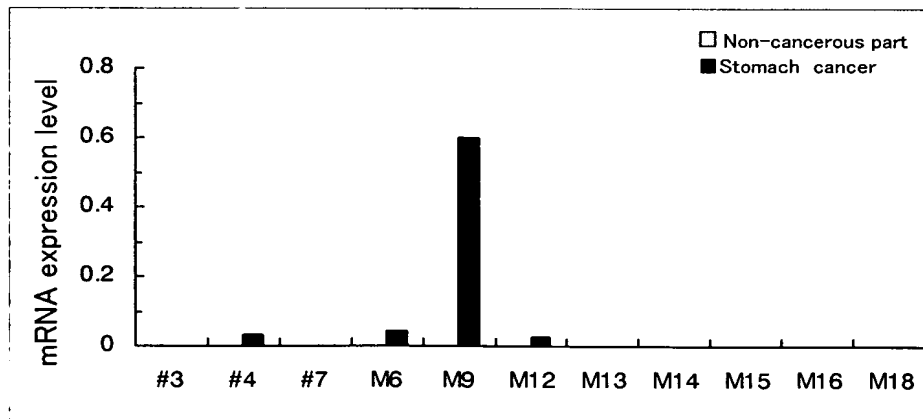


FIG. 26

## TEG25

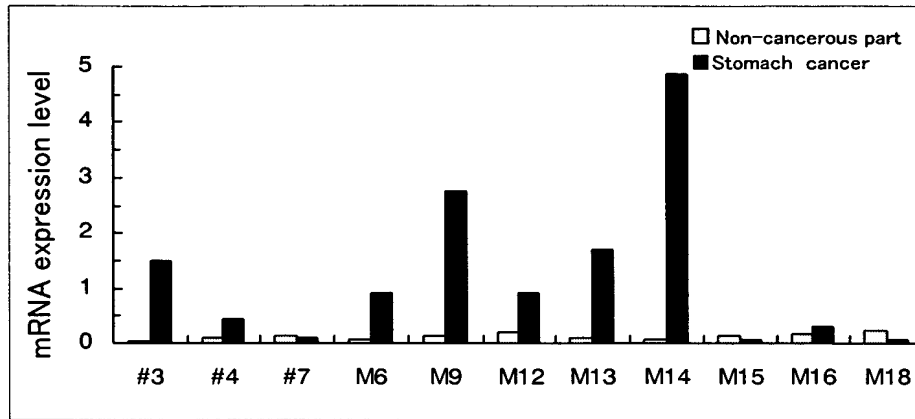


FIG. 27

## TEG26

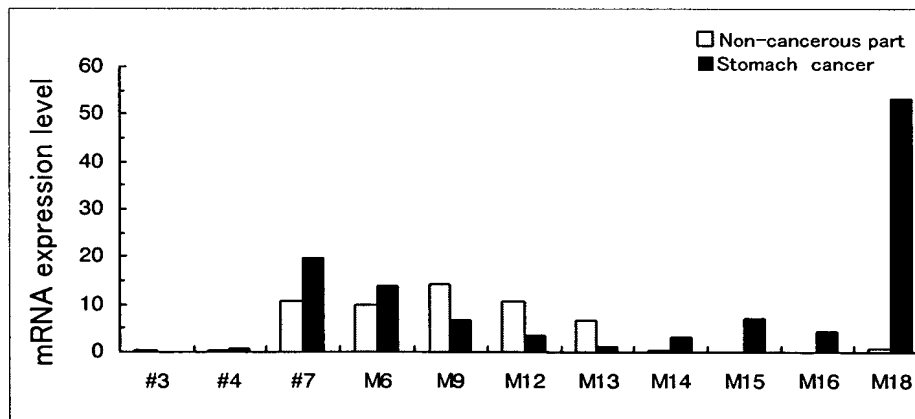


FIG. 28

TEG27

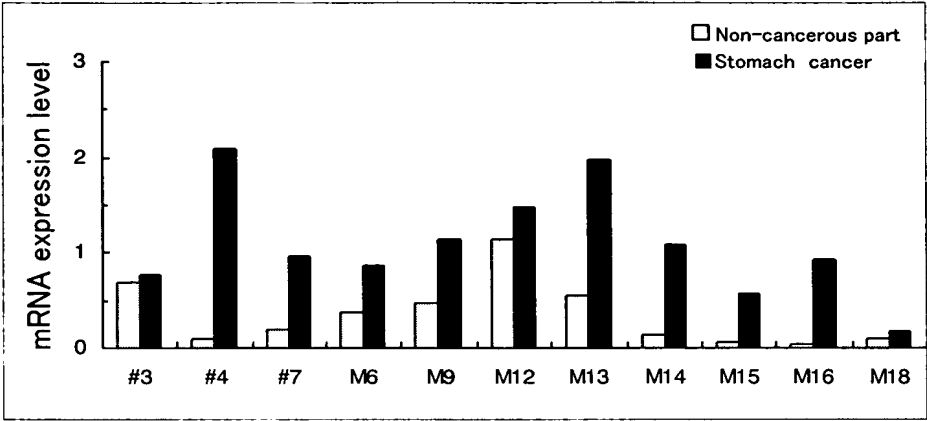


FIG. 29

TEG28

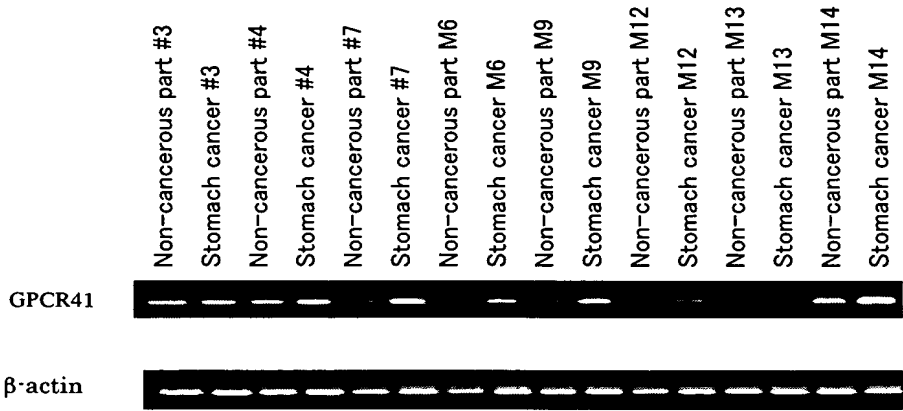


FIG. 30

## TEG29

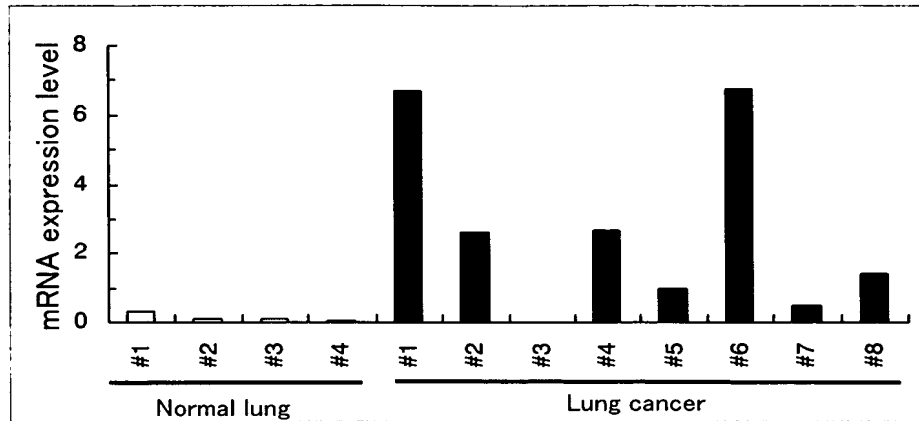


FIG. 31

## TEG30

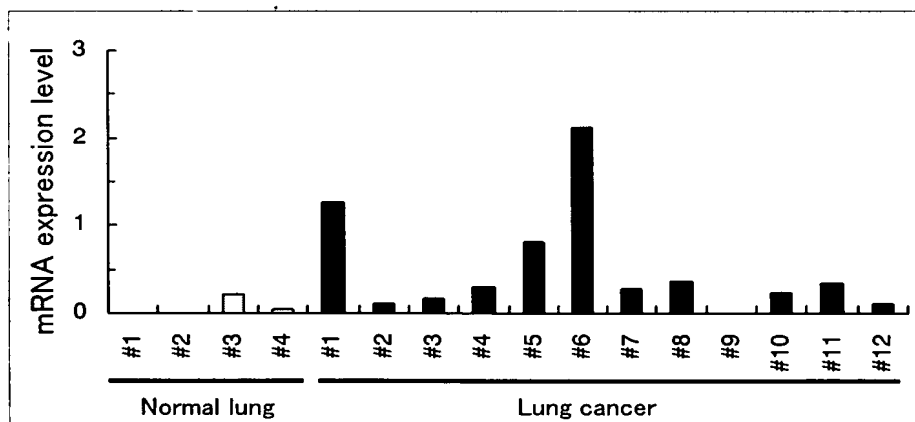


FIG. 32



## TEG31

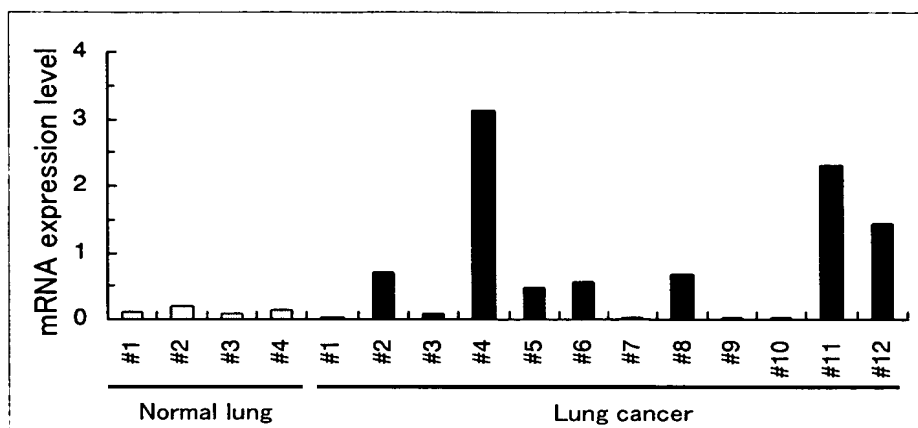


FIG. 33

## TEG32

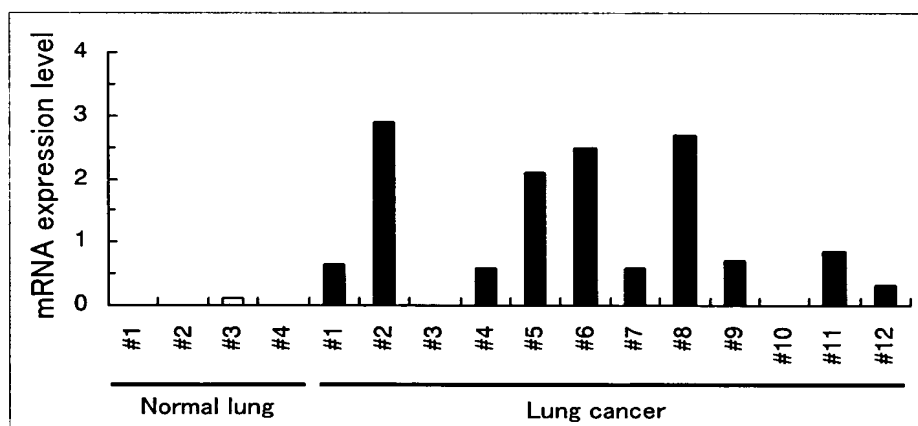


FIG. 34

## TEG33

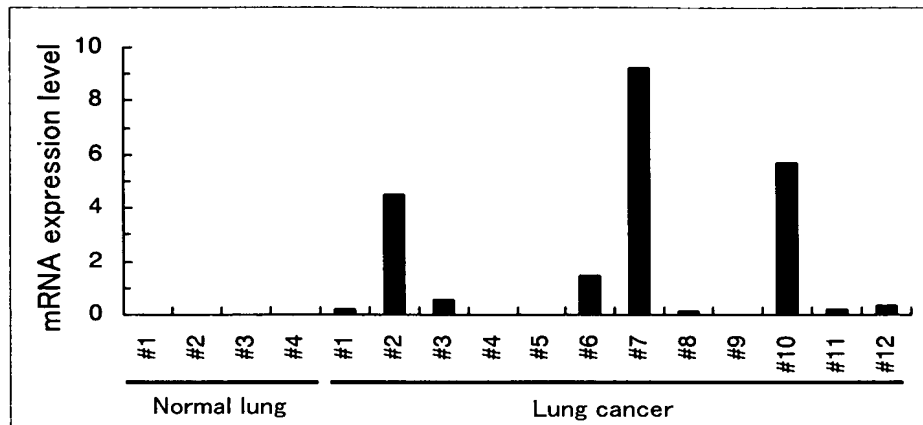


FIG. 35

## TEG34

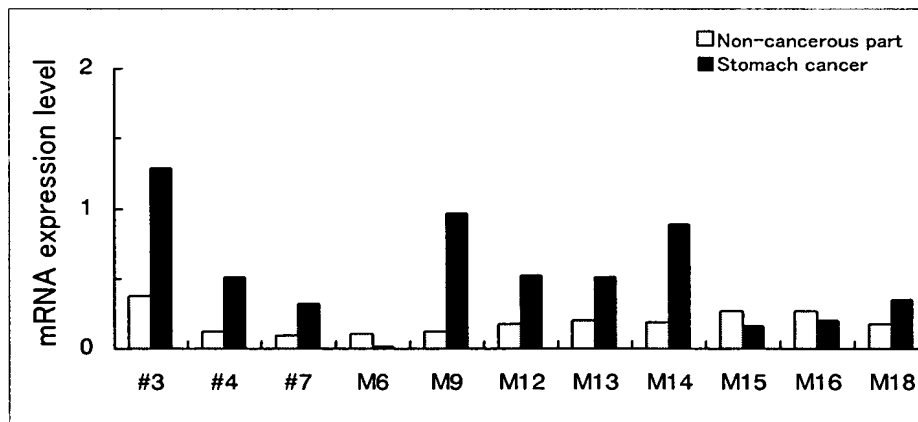


FIG. 36

19/66

### TEG35

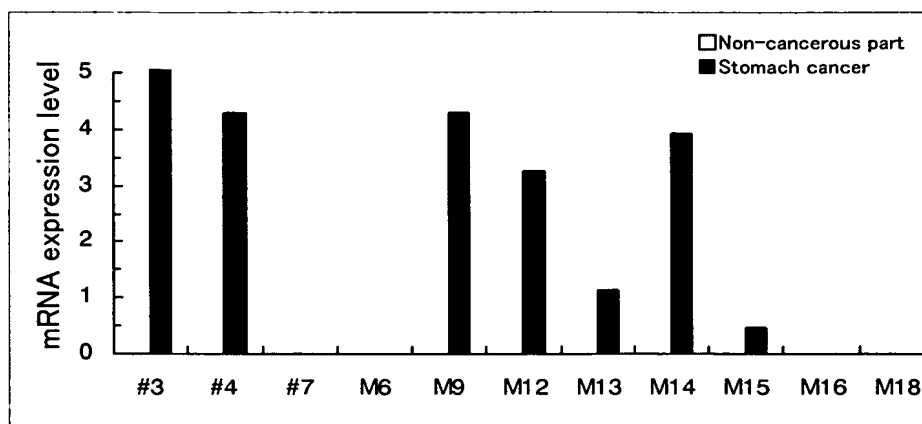


FIG. 37

### TEG36

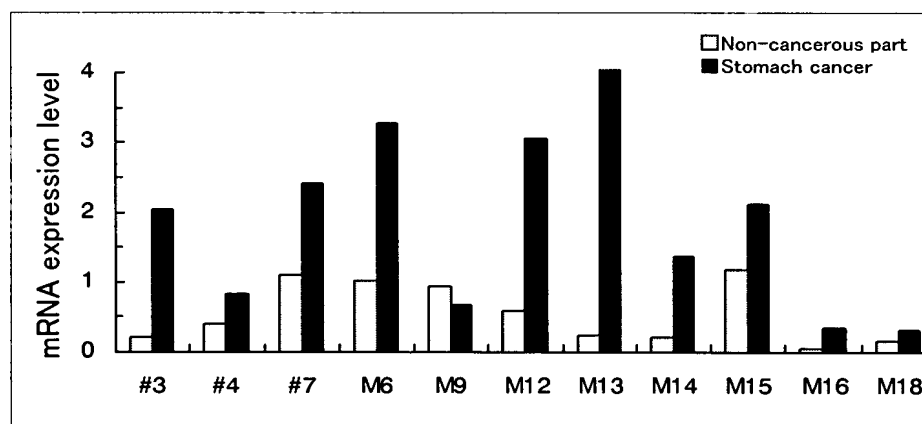


FIG. 38

## TEG37

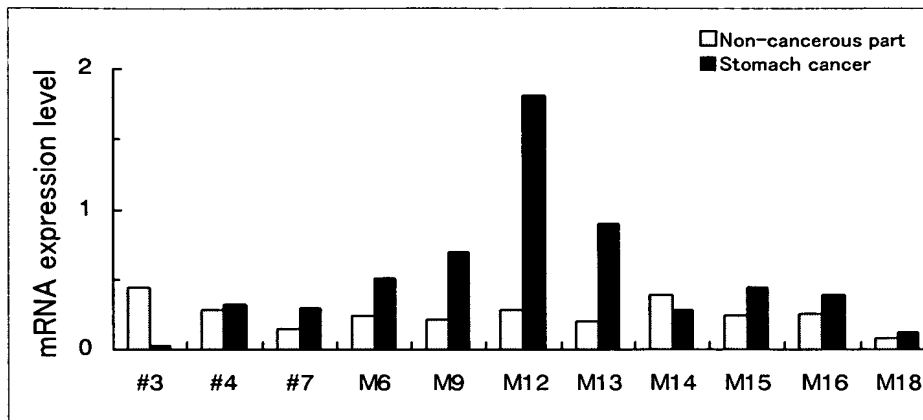


FIG. 39

## TEG38

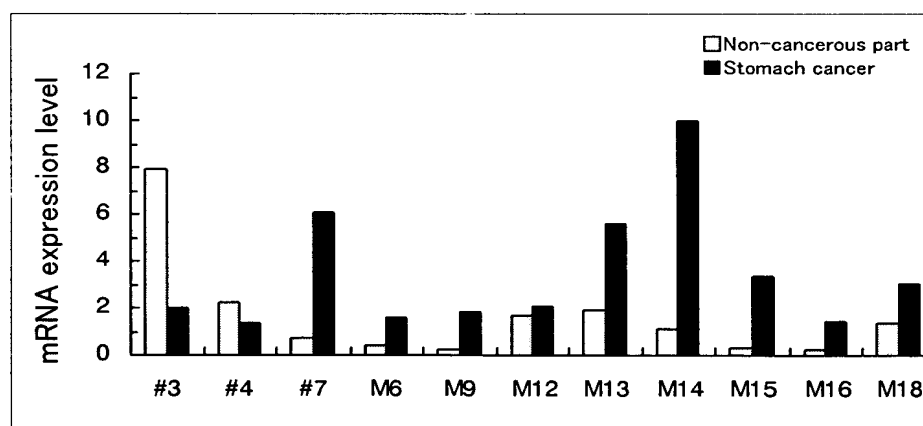


FIG. 40

## TEG39

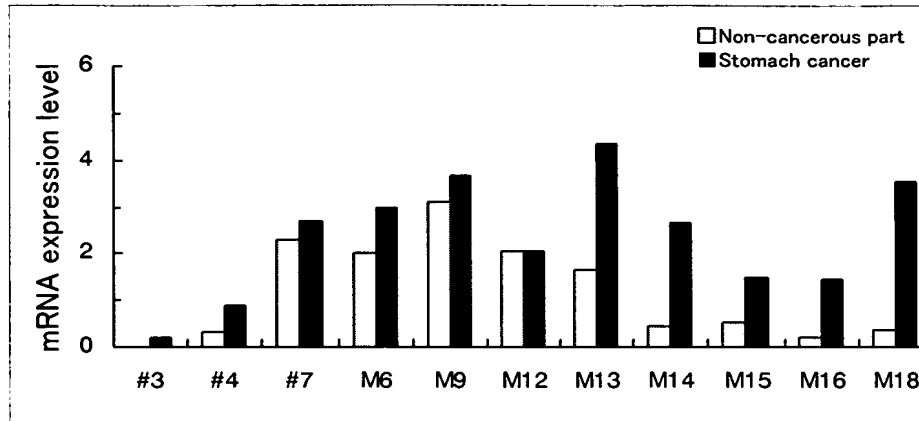


FIG. 41

## TEG40

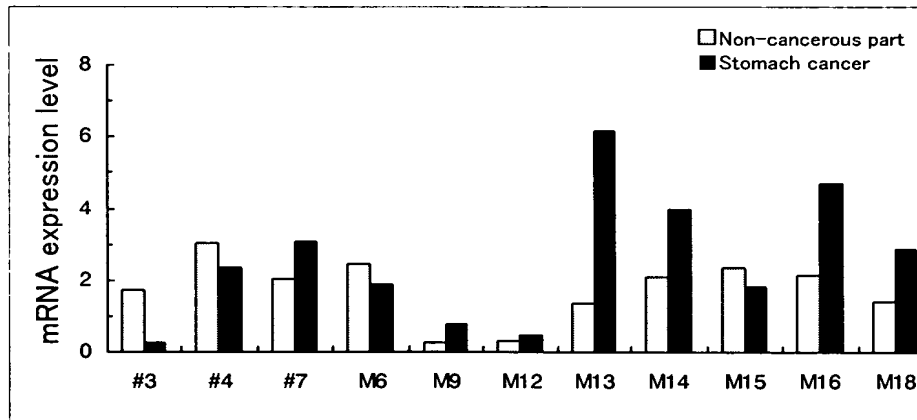


FIG. 42

## TEG41

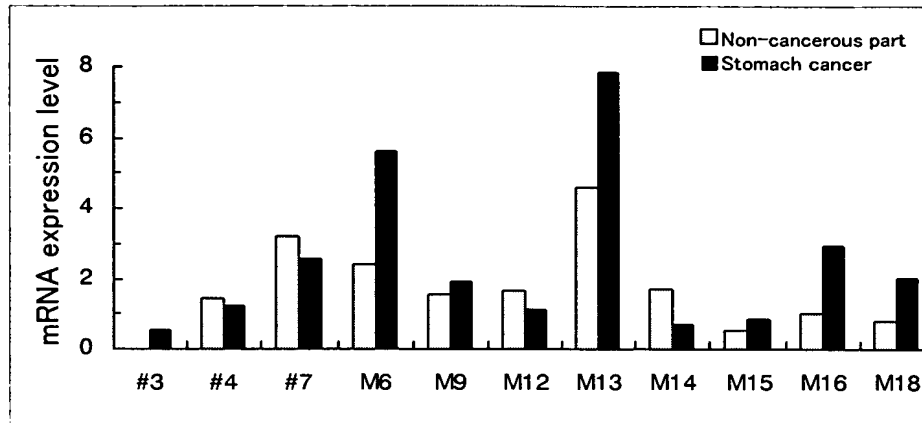


FIG. 43

## TEG42

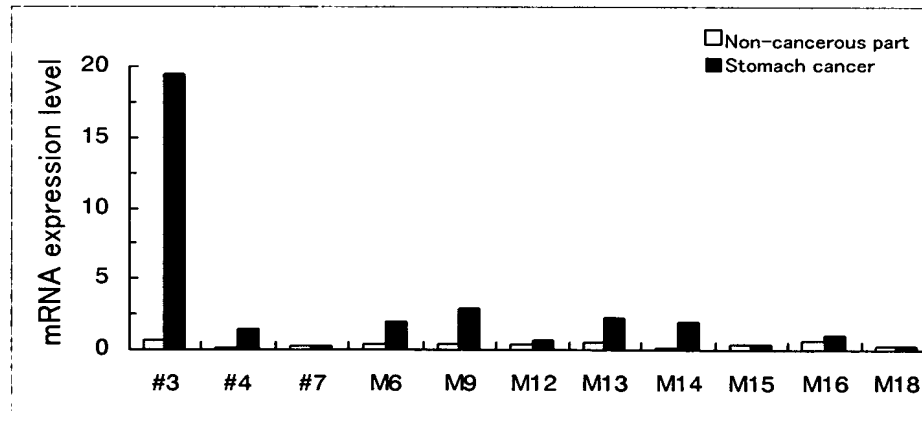


FIG. 44

## TEG43

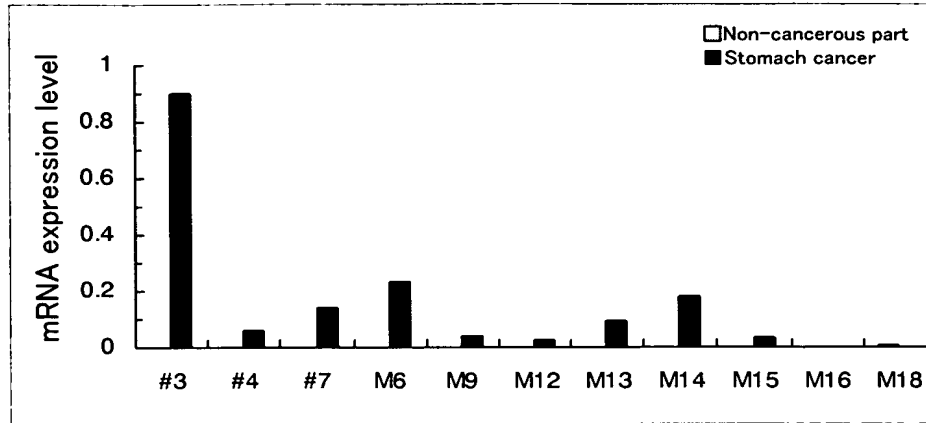


FIG. 45

## TEG44

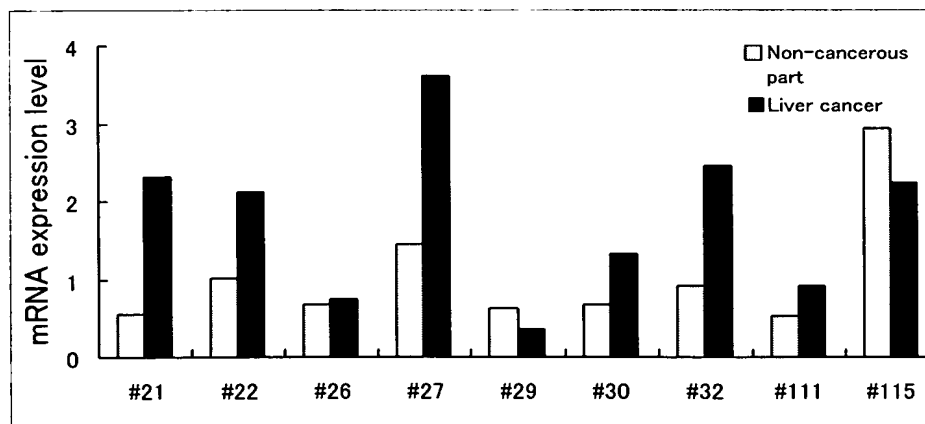


FIG. 46

## TEG45

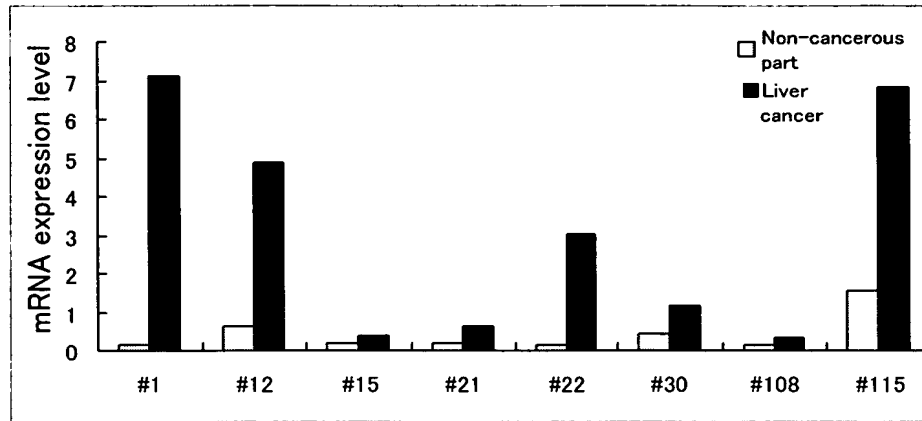


FIG. 47

## TEG46

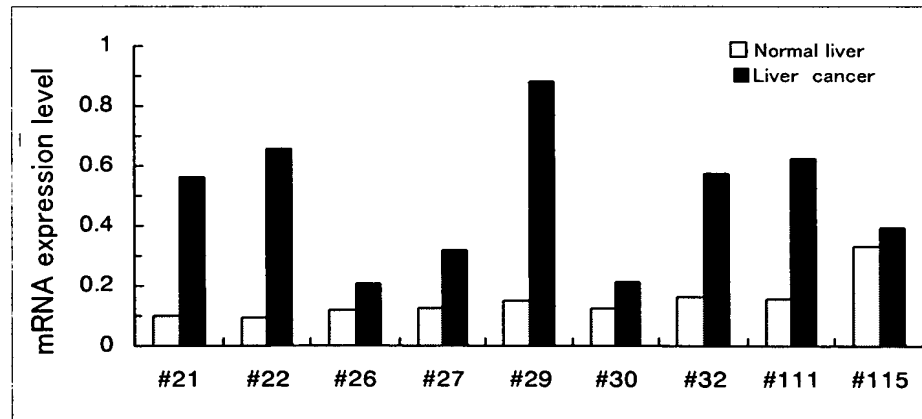


FIG. 48



## TEG47

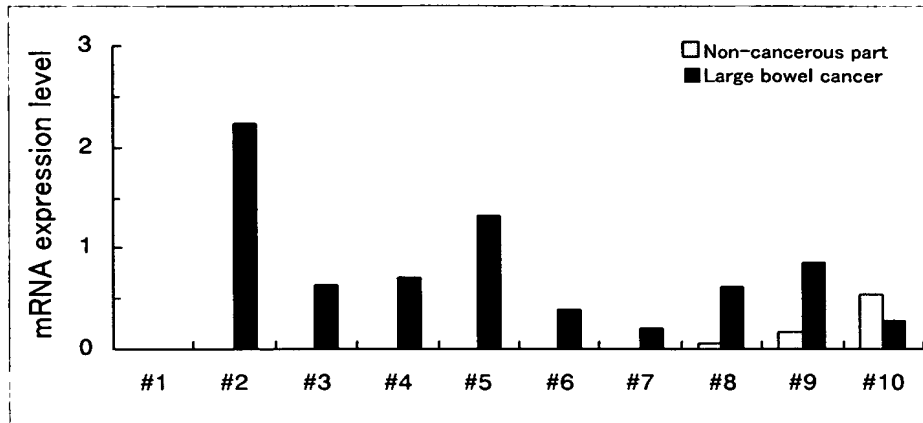


FIG. 49

## TEG48

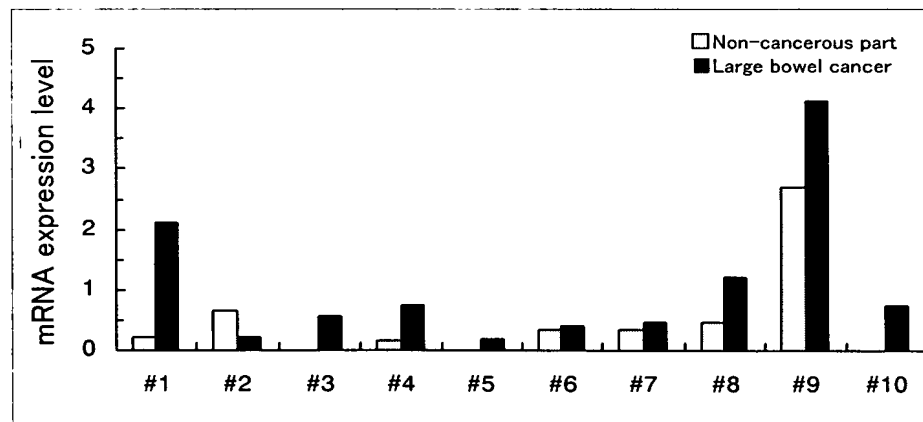


FIG. 50

## TEG49

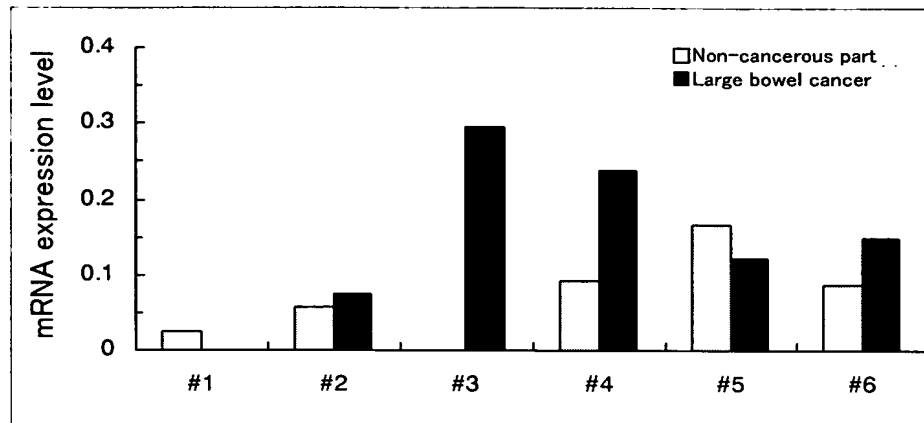


FIG. 51

## TEG50

TOP1MT

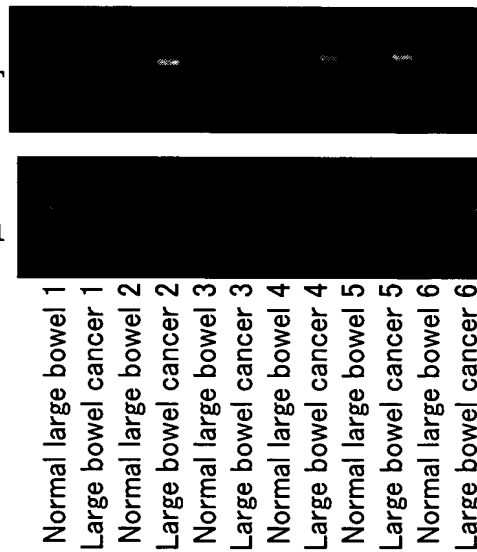
 $\beta$ -actin

FIG. 52

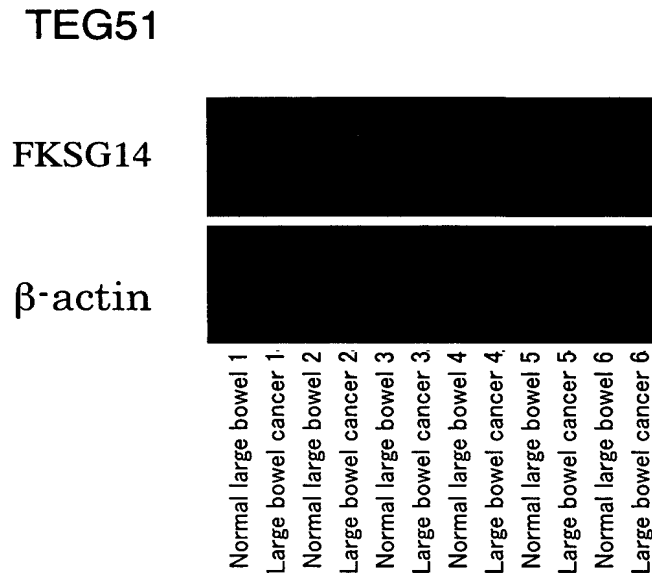


FIG. 53

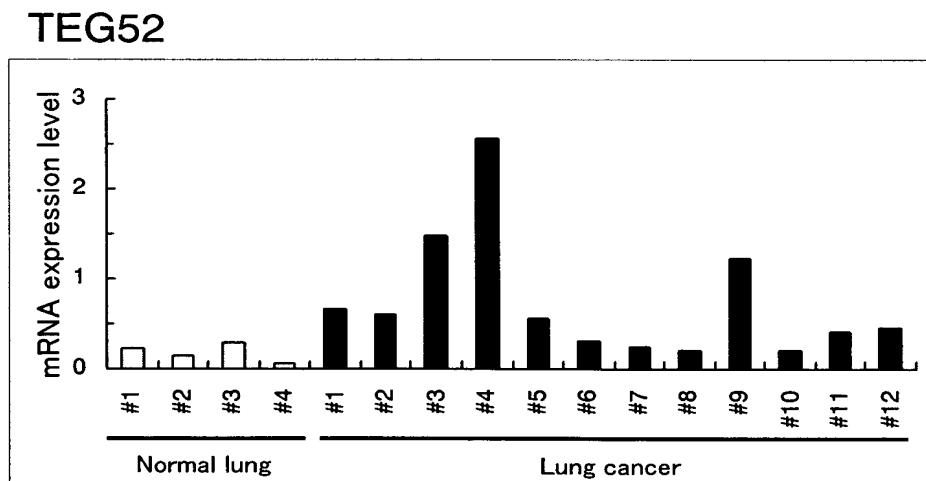


FIG. 54

## TEG53

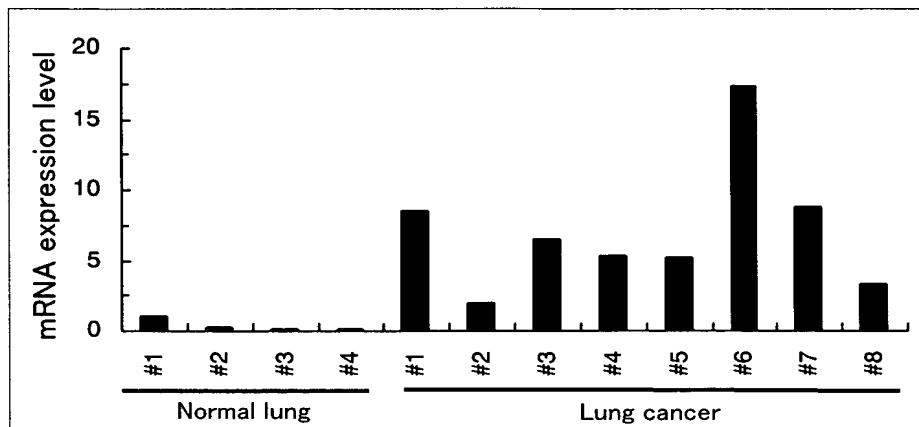


FIG. 55

## TEG54

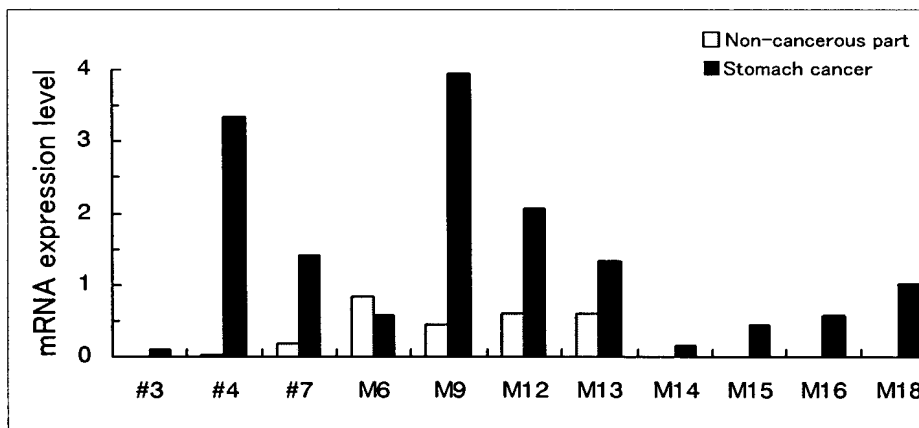


FIG. 56

## TEG55

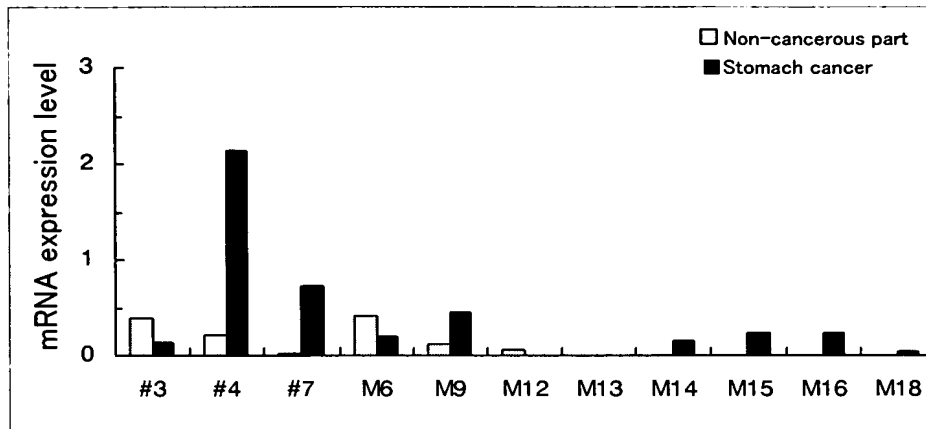


FIG. 57

## TEG56

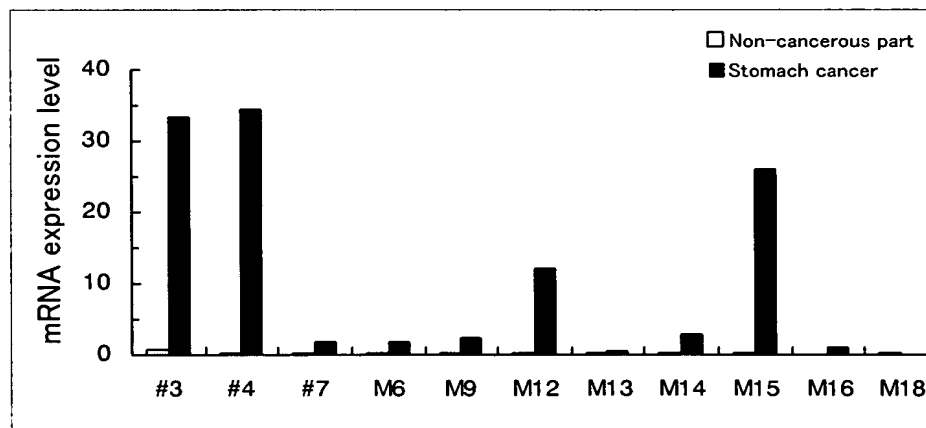


FIG. 58

## TEG57

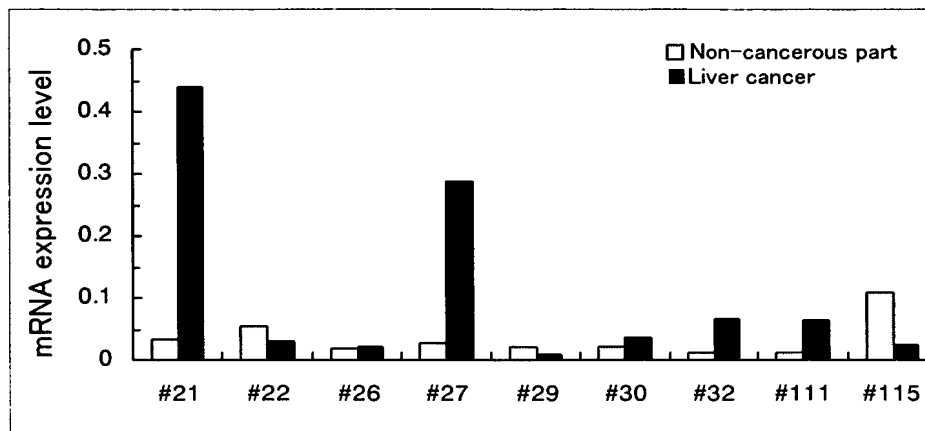


FIG. 59

## TEG58

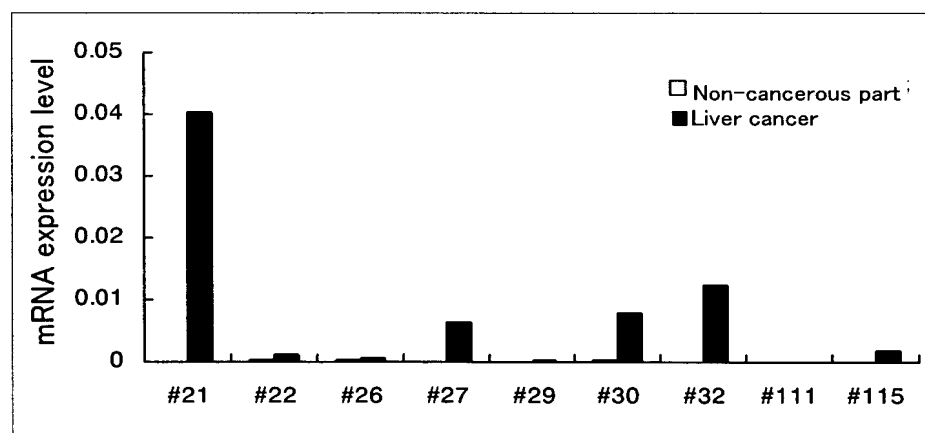


FIG. 60

## TEG59

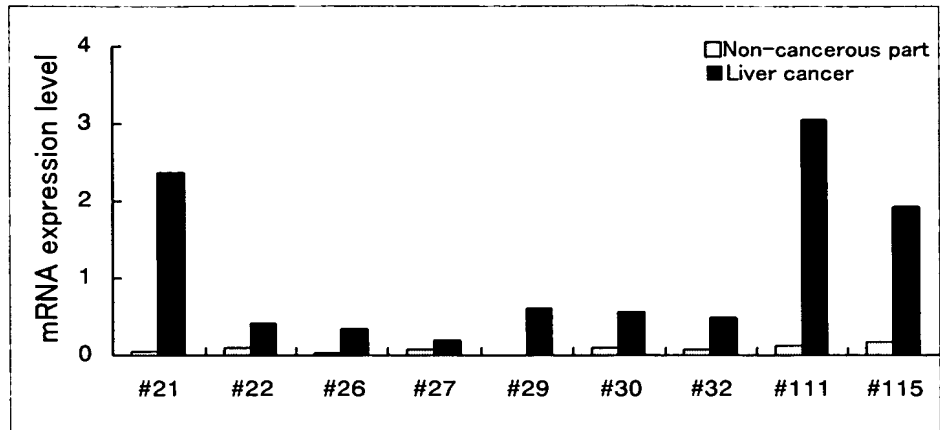


FIG. 61

## TEG60

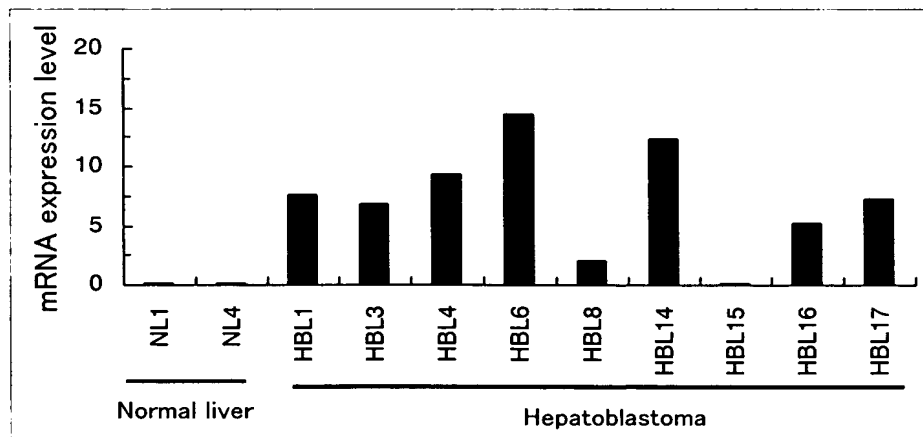


FIG. 62

## TEG61

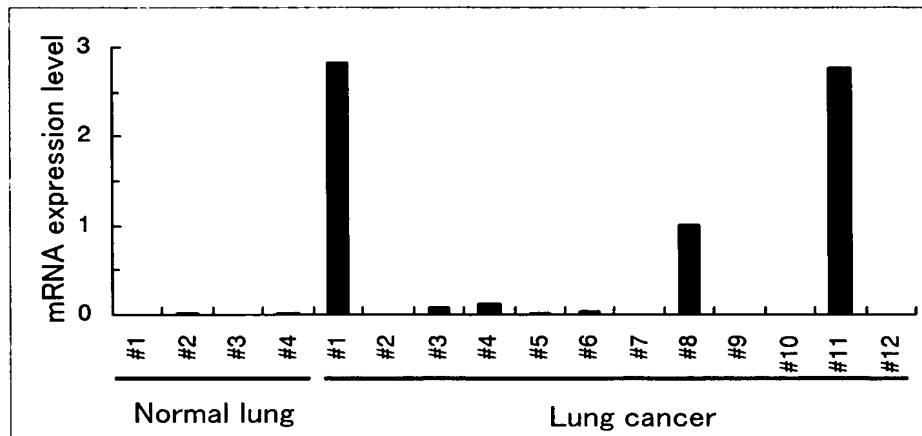


FIG. 63

## TEG62

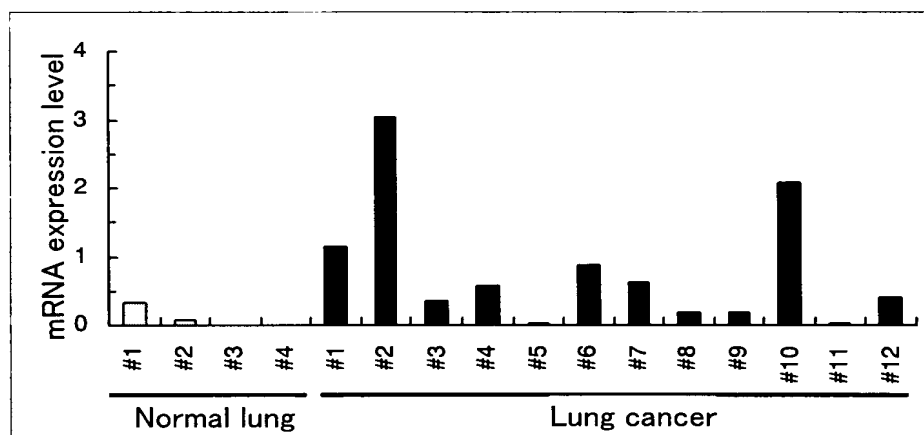


FIG. 64



## TEG63

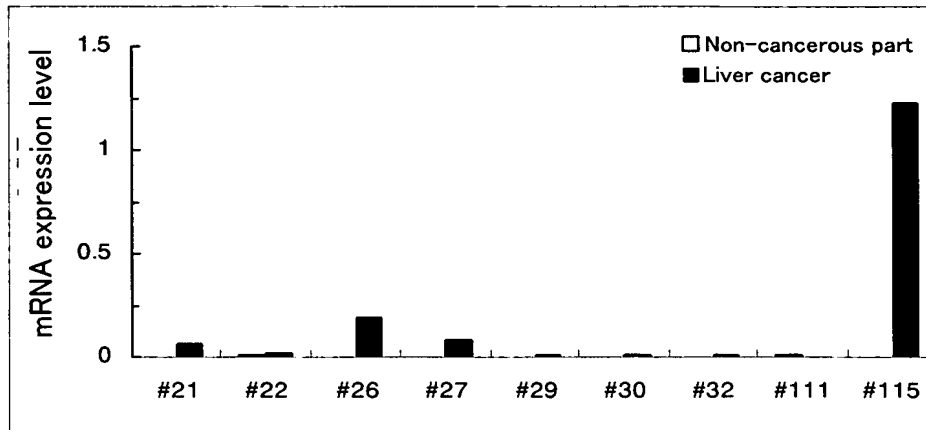


FIG. 65

## TEG64

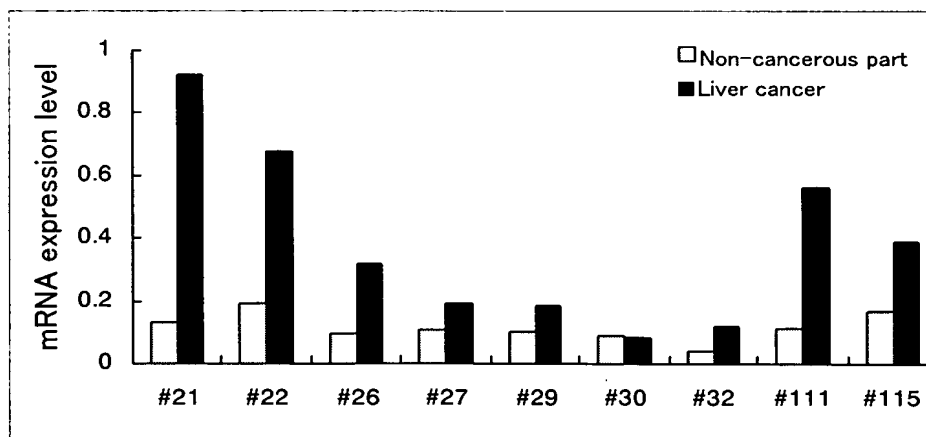


FIG. 66

ATGGCTTCGTTCCCCGAGACCGATTTCCAGATCTGCTTGCTGTGCAAGGAGATGTGCGGC	60
MetAlaSerPheProGluThrAspPheGlnIleCysLeuLeuCysLysGluMetCysGly	20
TCGCCGGCGCCGCTCTCCTCCAACCTCGTCCGCGTCGTCGTCTCTCGCAGACGTCCACG	120
SerProAlaProLeuSerSerAsnSerSerAlaSerSerSerSerSerGlnThrSerThr	40
TCGTGCGGGGGCGGCGGGGGGCCCTGGGGCGGCGGCGCCGCTACACGTCTTGCCC	180
SerSerGlyGlyGlyGlyGlyGlyProGlyAlaAlaAlaArgArgLeuHisValLeuPro	60
TGCCTGCACGCCTTCTGCCGCCCCTGCCTCGAGGCGCACCGGCTGCCGGCGGCGGGCGGC	240
CysLeuHisAlaPheCysArgProCysLeuGluAlaHisArgLeuProAlaAlaGlyGly	80
GGCGCGGCGGGAGAGCCGCTCAAGCTGCGCTGCCCCGTGTGCGACCAGAAAGTAGTGCTA	300
GlyAlaAlaGlyGluProLeuLysLeuArgCysProValCysAspGlnLysValValLeu	100
GCCGAGGCGGCGGGTATGGACGCGCTGCCTTCGTCCGCTTCCTGCTTAACAACCTGCTC	360
AlaGluAlaAlaGlyMETAspAlaLeuProSerSerAlaPheLeuLeuAsnAsnLeuLeu	120
GACGCGGTGGTGGCCACTGCCGACGAGCCGCCGCCAAGAACGGGCGCGCCGGCGCTCCG	420
AspAlaValValAlaThrAlaAspGluProProProLysAsnGlyArgAlaGlyAlaPro	140
GCGGGAGCGGGCGGCCACAGCAACCACCGGCACCACGCTCACCACGCGCACCCGCGCGCG	480
AlaGlyAlaGlyGlyHisSerAsnHisArgHisHisAlaHisHisAlaHisProArgAla	160
TCCGCCTCCGCGCCGCGCCACTCCCGCAGGCGCCGCGAGCCGCCCGCGCTTCCCGCTCGGCA	540
SerAlaSerAlaProProLeuProGlnAlaProGlnProProAlaProSerArgSerAla	180
CCCGGCGGCCCTGCCGCTTCCCCGTCGGCGCTGCTGCTCCGCCGTCTTCACGGCTGCAGC	600
ProGlyGlyProAlaAlaSerProSerAlaLeuLeuLeuArgArgProHisGlyCysSer	200
TCGTGCGATGAGGGCAACGCAGCTTCTTCGCGCTGCCTCGACTGCCAGGAGCACCTGTGC	660
SerCysAspGluGlyAsnAlaAlaSerSerArgCysLeuAspCysGlnGluHisLeuCys	220
GACAACTGCGTCCGAGCGCACCCAGCGCGTGCGCCTCACCAAGGACCACTACATCGAGCGC	720
AspAsnCysValArgAlaHisGlnArgValArgLeuThrLysAspHisTyrIleGluArg	240
GGCCCCCGGGTCCCGGTGCCGCGAGCAGCGGCGCAGCAGCTCGGGCTCGGGCCGCCCTTT	780
GlyProProGlyProGlyAlaAlaAlaAlaAlaGlnGlnLeuGlyLeuGlyProProPhe	260
CCCGGCCCGCCCTTCTCCATCCTCTCAGTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCAC	840
ProGlyProProPheSerIleLeuSerValPheProGluArgLeuGlyPheCysGlnHis	280

FIG. 67

CACGACGACGAGGTGCTGCACCTGTACTGTGACACTTGCTCTGTACCCATCTGTTCGTGAG 900  
HisAspAspGluValLeuHisLeuTyrCysAspThrCysSerValProIleCysArgGlu 300  
  
TGCACAATGGGCGGCATGGGGGCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGAC 960  
CysThrMetGlyArgHisGlyGlyHisSerPheIleTyrLeuGlnGluAlaLeuGlnAsp 320  
  
TCACGGGCACTCACCATCCAGCTGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAG 1020  
SerArgAlaLeuThrIleGlnLeuLeuAlaAspAlaGlnGlnGlyArgGlnAlaIleGln 340  
  
CTGAGCATCGAGCAGGCCAGACGGTGGCGGAACAGGTGGAGATGAAGGCGAAGGTTGTG 1080  
LeuSerIleGluGlnAlaGlnThrValAlaGluGlnValGluMetLysAlaLysValVal 360  
  
CAGTCGGAGGTCAAAGCCGTGACTGCGAGGCATAAGAAAGCCCTGGAGGAACGCGAGTGT 1140  
GlnSerGluValLysAlaValThrAlaArgHisLysLysAlaLeuGluGluArgGluCys 380  
  
GAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACCTGCAG 1200  
GluLeuLeuTrpLysValGluLysIleArgGlnValLysAlaLysSerLeuTyrLeuGln 400  
  
GTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGCAGCAG 1260  
ValGluLysLeuArgGlnAsnLeuAsnLysLeuGluSerThrIleSerAlaValGlnGln 420  
  
GTCCTGGAGGAGGGTAGAGCGCTAGACATCCTACTGGCCCGAGACCGGATGCTGGCCCAG 1320  
ValLeuGluGluGlyArgAlaLeuAspIleLeuLeuAlaArgAspArgMetLeuAlaGln 440  
  
GTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCCAGGAAGACGACCGAGTCATG 1380  
ValGlnGluLeuLysThrValArgSerLeuLeuGlnProGlnGluAspAspArgValMet 460  
  
TTCACACCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTTGGCTTTGTTAGCAGC 1440  
PheThrProProAspGlnAlaLeuTyrLeuAlaIleLysSerPheGlyPheValSerSer 480  
  
GGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCCAGGGT 1500  
GlyAlaPheAlaProLeuThrLysAlaThrGlyAspGlyLeuLysArgAlaLeuGlnGly 500  
  
AAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCTCAGGA 1560  
LysValAlaSerPheThrValIleGlyTyrAspHisAspGlyGluProArgLeuSerGly 520  
  
GGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGCAGAGGTG 1620  
GlyAspLeuMetSerAlaValValLeuGlyProAspGlyAsnLeuPheGlyAlaGluVal 540  
  
AGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCCAGCTGGAGGGTGAGCAC 1680  
SerAspGlnGlnAsnGlyThrTyrValValSerTyrArgProGlnLeuGluGlyGluHis 560

FIG. 67 (continued from previous page)

CTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGGTGGTC 1740  
 LeuValSerValThrLeuCysAsnGlnHisIleGluAsnSerProPheLysValValVal 580

AAGTCAGGCCCGCAGCTACGTGGGCATTGGGCTCCCGGGCCTGAGCTTCGGCAGTGAGGGT 1800  
 LysSerGlyArgSerTyrValGlyIleGlyLeuProGlyLeuSerPheGlySerGluGly 600

GACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCTACATC 1860  
 AspSerAspGlyLysLeuCysArgProTrpGlyValSerValAspLysGluGlyTyrIle 620

ATTGTCGCGCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCTTCCAC 1920  
 IleValAlaAspArgSerAsnAsnArgIleGlnValPheLysProCysGlyAlaPheHis 640

CACAAATTCCGGCACCCCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCGTGGCC 1980  
 HisLysPheGlyThrLeuGlySerArgProGlyGlnPheAspArgProAlaGlyValAla 660

TGTGACGCCTCACGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGATCTTC 2040  
 CysAspAlaSerArgArgIleValValAlaAspLysAspAsnHisArgIleGlnIlePhe 680

ACGTTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGCAGTTC 2100  
 ThrPheGluGlyGlnPheLeuLeuLysPheGlyGluLysGlyThrLysAsnGlyGlnPhe 700

AACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACACGAGG 2160  
 AsnTyrProTrpAspValAlaValAsnSerGluGlyLysIleLeuValSerAspThrArg 720

AACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCCTAAACAAGTATGGCTTCGAG 2220  
 AsnHisArgIleGlnLeuPheGlyProAspGlyValPheLeuAsnLysTyrGlyPheGlu 740

GGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGGTGTGGCCTTCAACCATGAGGGCCAC 2280  
 GlyAlaLeuTrpLysHisPheAspSerProArgGlyValAlaPheAsnHisGluGlyHis 760

TTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTCACCCCGACTGCCAGTCG 2340  
 LeuValValThrAspPheAsnAsnHisArgLeuLeuValIleHisProAspCysGlnSer 780

GCACGCTTTCTGGGCTCGGAGGGGCACAGGCAATGGGCAGTTCCTGCGCCCACAAGGGGTA 2400  
 AlaArgPheLeuGlySerGluGlyThrGlyAsnGlyGlnPheLeuArgProGlnGlyVal 800

GCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTACAGATG 2460  
 AlaValAspGlnGluGlyArgIleIleValAlaAspSerArgAsnHisArgValGlnMet 820

TTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTGGGCAG 2520  
 PheGluSerAsnGlySerPheLeuCysLysPheGlyAlaGlnGlySerGlyPheGlyGln 840

FIG. 67 (continued from previous page)

[illegible]

FIG. 67 (continued from previous page)

```

K#1. nuc      1:----- 1
XM_067369. nuc 1:ATGCGCGGACTGACCCAGCGGCCGCGCGCGCGCGCGGCGGACTTAATCGCGGGCGCA 60

K#1. nuc      1:----- 1
XM_067369. nuc 61:GCGCGAGGCTCGGGACCCAGAGCACCACCTACCGCGGCACGGTCGGCGCAGCAGGCCCC 120

K#1. nuc      1:----- 1
XM_067369. nuc 121:AGAAGGGCGGGGAACGCTGTCAAGCCCAGGGGCACTTCGGCGAGGAGCCCCACCCGCCCT 180

K#1. nuc      1:----- 1
XM_067369. nuc 181:CCAGCTGACCCTCAGCTGTGGCCACATCCGGGGCCAGAGCGCCGCGAAACGCCGAAG 240

K#1. nuc      1:----- 1
XM_067369. nuc 241:CCCGGCCGGCAGATAGCGCGGAAAGCGAAGAAGGAAGTTCCCGTCCCTCCTAAAGCCGAA 300

K#1. nuc      1:----- 1
XM_067369. nuc 301:GCCAAAGCGAAGTCTTTAAAGCCAAGAAGGCAGTGTGAAAGGTGTCCGCAGCCACAAA 360

K#1. nuc      1:----- 1
XM_067369. nuc 361:AAAAAGAAGATCCGCACGTACCCACCTTACGGCGGCCCAAGACACCGCGACTCCGGAGA 420

K#1. nuc      1:-----CCCTCCTCGGGCTGGGTTGCAAATGGCTTCGTTCCCGAGACCGATT 48
                  * *** * ** * * * ** ** * *
XM_067369. nuc 421:CAGCCCAAATATC-CTCGGAAGAGCGCTCCTAGGAGAAACAAGCTTGACCACTATGCTAT 479

K#1. nuc      49:TCCAGATCTGCTTGCTGTGCAAGGAGATGTGCGGCTCGCCGGCGCGCTCTCCTCCAAC 108
                  * * ** * ** *** * * * * **
XM_067369. nuc 480:CATCAAGTTTCTGCT-GACCACTGAGTCTGCCATGAAGAAGATAGAAGACAATAACACAC 538

K#1. nuc      109:C-GTCCGCGTCGTCGTCCTCCTCGCAGACGTCCACGTGTCGGGGGCGGCGCGGGGGC 167
                  ** * * ** * * ** ** *** * * * * **
XM_067369. nuc 539:TTGTGTTCAATTGTGGATGTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGC 598

K#1. nuc      168:CCTGGGGCGGCGCGCGCCGCTACACGTCCTGCCCTGCCTGCACGCCTTCTGCCGCCCC 227
                  ** * * * * * * * * * *
XM_067369. nuc 599:TCTATGACAAAGATGTGGTCAAGGTCAACACCCTGATTTCGGCCTGATGGAGAGAAGAAG 658

K#1. nuc      228:TGCCTCGAGGCGCACCGGCTGCCGGCGGGGCGGCGGCGGCGGAGAGCCGCTCAAG 287
                  *** * * ** ** ** * * * ** * * *
XM_067369. nuc 659:CGCCGCAGCCGCCCGCCTTCCCGCTCGGCACCCGGCGGCCCTGCCGCTTCCCCGTCGG 718

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FIG. 68

K#1. nuc 288:CTGCGCTGCCCCGTGTGCGACCAGAAAGTAGTGCTAGCCGAGGCGGGTATGGACGCG 347  
 \* \*\*\*\*\* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 719:CGCTGCTGCTCCGCCGTCCTCAGGCTGCAGCTCGTGCGATGAGGGCAACGCAGCTTCTT 778  
  
 K#1. nuc 348:CTGCCTTCGTCCGCTTCCTGCTTAACAACCTGCTCGACGCGGTGGTGGCCACTGCCGAC 407  
 \* \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 779:CGCGCTGCCTCGACTGCCAGGAGCACCTGTGCGACAACTGCGTCCGAGCGCACCAGCGCG 838  
  
 K#1. nuc 408:GAGCCGCCGCCAAGAACGGGCGCGCCGGCGCTCCGGCGGGAGCGGGCGGCCAC-AGCAA 466  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 839:TGCGCCTCACCAAGGACCACTACATCGAGCGCGGCCCGCGGGTCCCGGTGCCGAGCAG 898  
  
 K#1. nuc 467:CCACCGGCACCACGCTCACCACGCGCACCCGCGCGCTCCGCCTCCGCGCCGCACTCCC 526  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 899:CGGCGCAG-CAGCTCGGGCTCGGGCGGCCCTTTCCCGGCCCGCCCTTCTCCATCCTCTCA 957  
  
 K#1. nuc 527:GCAGGCGCCGAGCCGCCCGCGCCTTCCCGCTCGGCACCCGGCGGCCCTGCCGCTTCCCC 586  
 \* \*\*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 958:GTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCACCACGACGACGAGTTGGGGCTTTTCACT 1017  
  
 K#1. nuc 587:GTCGGCGCTGCTGCTCCGCCGTCTCAGGCTGCAGCTCGTGCGATGAGGGCAACGCAG- 645  
 \* \*\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 1018:AGTTCTGTGCTCCAGAGTCCGAAAGGCTGCAGGCTCCGTGGCCAGCCGGCATCCGGG 1077  
  
 K#1. nuc 646:CTTCTTCGCGCTGCCTCGACTGCCAGGAGCACCTGTGCGACAACTGCGTCCGAGCGCACC 705  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 1078:CGGGGAATCCAAGGCGAGGAATCCGAGGTCGCCGTCCCCGGAACAGCTGGCCGCGGGCCC 1137  
  
 K#1. nuc 706:AGCGCGTGCGCCTACCAAGGACCACTACATCGAGCGCGGCCCGCGGGTCCCGGTGCCG 765  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 1138:GCTGCGTGCCGCGGGTCCCGGGAGAGCGGGCGCAGGCTAGAGCAGCAAAGGAACTTTT 1197  
  
 K#1. nuc 766:CAGCAGCGGCGCAGCAGCTCGGGCTCGGGCCGCCCTTTCCCGGCCCGCCCTTCTCCATCC 825  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 1198:CTGGTACATTCTTACATCCAGGCCACTAATATCAGACTAGGTAACACAGTCTTAACAAC 1257  
  
 K#1. nuc 826:TCTCAGTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCACCACGACGAGGTGCTGCACC 885  
 \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
 XM\_067369. nuc 1258:TTTCTGATAATGAAGCTAAGATTAGGGCAAACCTCTCATGCCAGGAGG--TGCTGCACC 1315

FIG. 68 (continued from previous page)

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K#1. nuc      886:TGTA CTGTGACACTTGCTCTGTACCCATCTGTCGTGAGTGCACAATGGGCCGGCATGGGG 945
      *****
XM_067369. nuc 1316:TGTA CTGTGACACTTGCTCTGTACCCATCTGTCGTGAGTGCACAATGGGCCGGCATGGGG 1375

K#1. nuc      946:GCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGACTCACGGGCACTCACCATCCAGC 1005
      *****
XM_067369. nuc 1376:GCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGACTCACGGGCACTCACCATCCAGC 1435

K#1. nuc      1006:TGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAGCTGA----- 1047
      ***** *
XM_067369. nuc 1436:TGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAGACAAAGCAGAAGAAGCTGCTTC 1495

K#1. nuc      1048:-----GCATCGAGCAGGCCAGCGGTGGCGGAACAGGTGGAGATGAAGGCCAAGG 1098
      *****
XM_067369. nuc 1496:TGCAGCTGAGCATCGAGCAGGCCAGCGGTGGCGGAACAGGTGGAGATGAAGGCCAAGG 1555

K#1. nuc      1099:TTGTGCAGTCGGAGGTCAAAGCCGTGACTGCGAGGCATAAGAAAGCCCTGGAGGAACGCG 1158
      *****
XM_067369. nuc 1556:TTGTGCAGTCGGAGGTCAAAGCCGTGACGGCGAGGCATAAGAAAGCCCTGGAGGAACGCG 1615

K#1. nuc      1159:AGTGTGAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACC 1218
      *****
XM_067369. nuc 1616:AGTGTGAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACC 1675

K#1. nuc      1219:TGCAGGTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGC 1278
      *****
XM_067369. nuc 1676:TGCAGGTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGC 1735

K#1. nuc      1279:AGCAGGTCCTGGAGGAGGTAGAGCGCTAGACATCCTACTGGCCCAGACCGGATGCTGG 1338
      *****
XM_067369. nuc 1736:AGCAGGTCCTGGAGGAGGTAGAGCGCTAGACATCCTACTGGCCCAGACCGGATGCTGG 1795

K#1. nuc      1339:CCCAGGTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCAGGAAGACGACCGAG 1398
      *****
XM_067369. nuc 1796:CCCAGGTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCAGGAAGACGACCGAG 1855

K#1. nuc      1399:TCATGTTACACCCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTGGCTTTGTTA 1458
      *****
XM_067369. nuc 1856:TCATGTTACACCCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTGGCTTTGTTA 1915

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FIG. 68 (continued from previous page)



K#1. nuc 1459:GCAGCGGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCC 1518  
 \*\*\*\*\*  
 XM\_067369. nuc 1916:GCAGCGGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCC 1975  
  
 K#1. nuc 1519:AGGGTAAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCT 1578  
 \*\*\*\*\*  
 XM\_067369. nuc 1976:AGGGTAAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCT 2035  
  
 K#1. nuc 1579:CAGGAGGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGAC 1638  
 \*\*\*\*\*  
 XM\_067369. nuc 2036:CAGGAGGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGAC 2095  
  
 K#1. nuc 1639:AGGTGAGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCAGCTGGAGGGTG 1698  
 \*\*\*\*\*  
 XM\_067369. nuc 2096:AGGTGAGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCAGCTGGAGGGTG 2155  
  
 K#1. nuc 1699:AGCACCTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGG 1758  
 \*\*\*\*\*  
 XM\_067369. nuc 2156:AGCACCTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGG 2215  
  
 K#1. nuc 1759:TGGTCAAGTCAGGCCGAGCTACGTGGGCATTGGGCTCCCGGCCTGAGCTTCGGCAGTG 1818  
 \*\*\*\*\*  
 XM\_067369. nuc 2216:TGGTCAAGTCAGGCCGAGCTACGTGGGCATTGGGCTCCCGGCCTGAGCTTCGGCAGTG 2275  
  
 K#1. nuc 1819:AGGGTGACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCT 1878  
 \*\*\*\*\*  
 XM\_067369. nuc 2276:AGGGTGACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCT 2335  
  
 K#1. nuc 1879:ACATCATTGTGCGCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCT 1938  
 \*\*\*\*\*  
 XM\_067369. nuc 2336:ACATCATTGTGCGCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCT 2395  
  
 K#1. nuc 1939:TCCACCACAAATTCGGCACCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCG 1998  
 \*\*\*\*\*  
 XM\_067369. nuc 2396:TCCACCACAAATTCGGCACCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCG 2455  
  
 K#1. nuc 1999:TGGCCTGTGACGCTCAGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGA 2058  
 \*\*\*\*\*  
 XM\_067369. nuc 2456:TGGCCTGTGACGCTCAGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGA 2515

FIG. 68 (continued from previous page)

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K#1. nuc      2059:TCTTCACGTTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGC 2118
               *****
XM_067369. nuc 2516:TCTTCACGTTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGC 2575

K#1. nuc      2119:AGTTCAACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACA 2178
               *****
XM_067369. nuc 2576:AGTTCAACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACA 2635

K#1. nuc      2179:CGAGGAACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCTAAACAAGTATGGCT 2238
               *****
XM_067369. nuc 2636:CGAGGAACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCTAAACAAGTATGGCT 2695

K#1. nuc      2239:TCGAGGGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGTGTGGCCTTCAACCATGAGG 2298
               *****
XM_067369. nuc 2696:TCGAGGGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGTGTGGCCTTCAACCATGAGG 2755

K#1. nuc      2299:GCCACTTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTACCCCGACTGCC 2358
               *****
XM_067369. nuc 2756:GCCACTTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTACCCCGACTGCC 2815

K#1. nuc      2359:AGTCGGCACGCTTTCTGGGCTCGGAGGGCACAGGCAATGGGCAGTTCCTGCGCCACAAG 2418
               *****
XM_067369. nuc 2816:AGTCGGCACGCTTTCTGGGCTCGGAGGGCACAGGCAATGGGCAGTTCCTGCGCCACAAG 2875

K#1. nuc      2419:GGGTAGCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTAC 2478
               *****
XM_067369. nuc 2876:GGGTAGCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTAC 2935

K#1. nuc      2479:AGATGTTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTG 2538
               *****
XM_067369. nuc 2936:AGATGTTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTG 2995

K#1. nuc      2539:GGCAGATGGACCGCCCTTCCGGCATCGCCATCACCCCGACGGAATGATCGTTGTGGTGG 2598
               *****
XM_067369. nuc 2996:GGCAGATGGACCGCCCTTCCGGCATCGCCATCACCCCGACGGAATGATCGTTGTGGTGG 3055

K#1. nuc      2599:ACTTTGGCAACAATCGAATCCTCGTCTTCTAATTGCATTTCCTAGTTTCTGTGTTGGG 2658
               *****
XM_067369. nuc 3056:ACTTTGGCAACAATCGAATCCTCGTCTTCTA----- 3087

K#1. nuc      2659:GTGTGTGTGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTTTGAATTT 2718
XM_067369. nuc 3088:----- 3088

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FIG. 68 (continued from previous page)

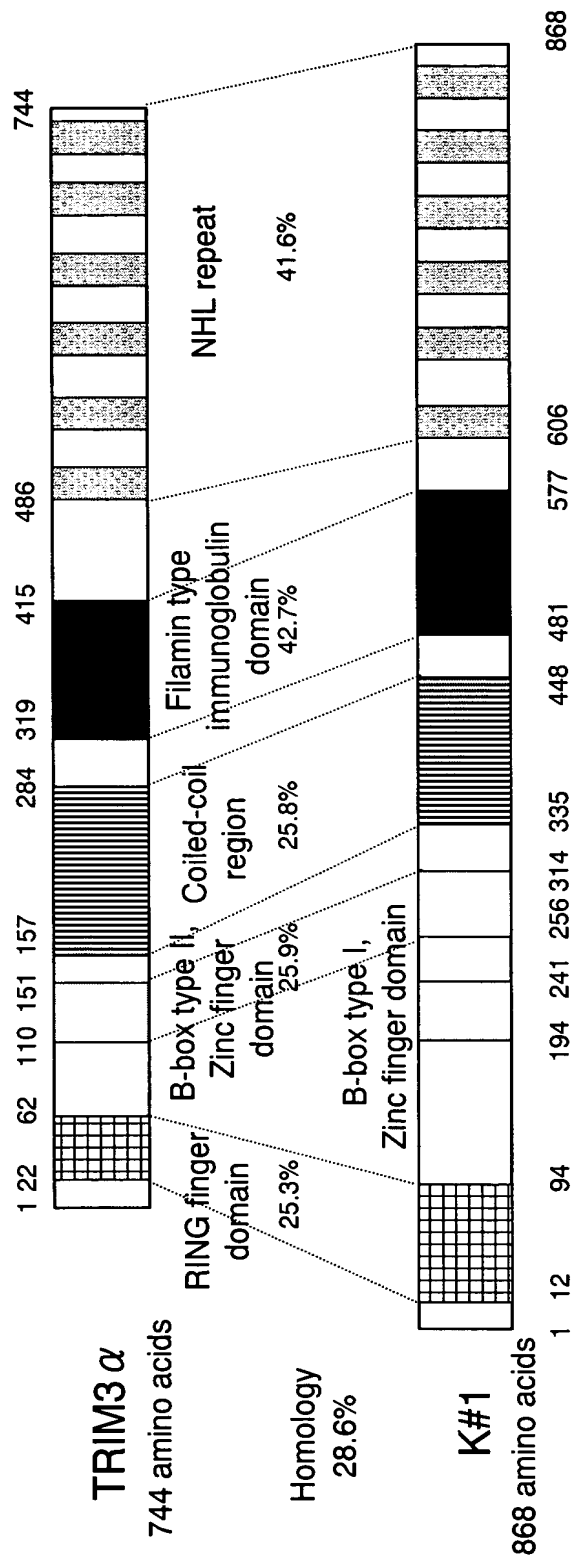


FIG. 69

GTAATTGACAAAGTCACGTGTGCTCAGGGGGCCAGAACTGGAGAGAGGAGAGAAAAAAA	60
TCAAAAGAAGGAAAGCACATTAGACCATGCGAGCTAAATTTGTGATCGCACAAAATCAAG	120
ATGTTAGATTGATGCAGAAGATCACTCCGTTCCAAAGGGAAAGTTTTTCATCTCACGAGTT	180
TGGAGCTGAGGGCCCGTGGGGCAACATGGCCGAAGGCGGGGCTAGCAAAGGTGGTGGAGA	240
MetAlaGluGlyGlyAlaSerLysGlyGlyGlyGlu	12
AGAGCCCGGGAAGCTGCCGGAGCCGGCAGAGGAGGAATCCCAGGTTTTGCGCGGAACTGG	300
GluProGlyLysLeuProGluProAlaGluGluGluSerGlnValLeuArgGlyThrGly	32
CCACTGTAAGTGGTTCAATGTGCGCATGGGATTTGGATTTCATCTCCATGATAAACCGAGA	360
HisCysLysTrpPheAsnValArgMetGlyPheGlyPheIleSerMetIleAsnArgGlu	52
GGGAAGCCCCTTGATATTCCAGTCGATGTATTTGTACACCAAAGCAAACCTATTCATGGA	420
GlySerProLeuAspIleProValAspValPheValHisGlnSerLysLeuPheMetGlu	72
AGGATTTAGAAGCCTAAAAGAAGGAGAACCAGTGAATTCACATTTAAAAAATCTTCCAA	480
GlyPheArgSerLeuLysGluGlyGluProValGluPheThrPheLysLysSerSerLys	92
AGGCCTTGAGTCAATACGGGTAACAGGACCTGGTGGGAGCCCCTGTTTAGGAAGTGAAAG	540
GlyLeuGluSerIleArgValThrGlyProGlyGlySerProCysLeuGlySerGluArg	112
AAGACCCAAAGGGAAGACACTACAGAAAAGAAAACCAAAGGGAGATAGATGCTACAACCTG	600
ArgProLysGlyLysThrLeuGlnLysArgLysProLysGlyAspArgCysTyrAsnCys	132
TGGTGGCCTTGATCATCATGCTAAGGAATGTAGTCTACCTCCTCAGCCAAAGAAGTGCCA	660
GlyGlyLeuAspHisHisAlaLysGluCysSerLeuProProGlnProLysLysCysHis	152
TTACTGTCAGAGCATCATGCACATGGTGGCAAACCTGCCCACATAAAAAATGTTGCACAGCC	720
TyrCysGlnSerIleMetHisMetValAlaAsnCysProHisLysAsnValAlaGlnPro	172
ACCCGCGAGTTCTCAGGGAAGACAGGAAGCAGAATCCCAGCCATGCACTTCAACTCTCCC	780
ProAlaSerSerGlnGlyArgGlnGluAlaGluSerGlnProCysThrSerThrLeuPro	192
TCGAGAAGTGGGAGGCGGGCATGGCTGTACATCACCACCGTTTCCTCAGGAGGCTAGGGC	840
ArgGluValGlyGlyGlyHisGlyCysThrSerProProPheProGlnGluAlaArgAla	212
AGAGATCTCAGAACGGTCAGGCAGGTCACCTCAAGAAGCTTCCTCCACGAAGTCATCTAT	900
GluIleSerGluArgSerGlyArgSerProGlnGluAlaSerSerThrLysSerSerIle	232
AGCACCAGAAGAGCAAAGCAAAAAGGGGCCTTCAGTTCAAAAAAGGAAAAAGACATAACA	960
AlaProGluGluGlnSerLysLysGlyProSerValGlnLysArgLysLysThr***	250

FIG. 70

GGTCTTCTTCATATGTTCTTTCCCTTTACCCGGTTGCAAAGTCTACCTCATGCAAGTATAG 1020  
GGGAACAGTATTTTACAAGCAGTAGCTGACCTGGGATTTTAACTACTATTGGGGAACTGT 1080  
GAATTTTTTTAAACAGACAAATCACTCTAAGCAAATTACATTTGAGCAGGGTGTCTATGTTT 1140  
TATGTTAATTCAGAGAATAAGATACTATGTCTGTCAATATGTGCATGTGTGAGAGGGAGA 1200  
GAGCCTGAGTCTGTGTGTGTACATGAGGATTTTATATAGGAATGTAGACACATATATAA 1260  
AGAGGCTTTGTCTTTATATATTTGTGTATAGATCAAAGCACACACCCCTCTCTCATATAAT 1320  
TGGATATTTCCAAGAATTGAAAACCCATGTGAAGCATTATAGATAGTTTAAATTTAACC 1380  
CACTGGAGTTTTCTTGAAATACCACTTCTTTTATATTATATAAACTAAAAACACGACTG 1440  
TTACCTTTTGTGTGAACCAAAGGATACTTCAGATCTCAGAGCTGCCAATTATGGGGTACT 1500  
AAAGGTTTTTTAAGACATCCAGTTCTCCCGAATTTGGGATTGCCTCTTTTTCTTGAAATCT 1560  
CTGGAGTAGTAATTTTTTTCCCCCTTTTTTGAAGGCAGTACCTTAACCTCATATGCCCTCT 1620  
GACTGCCATAAGCTTTTTTGAATTCTGGGATAACATAACTCCAGAAAAGACAATGAATGTG 1680  
TAATTTGGGCCGATATTTCACTGTTTTAAATTTCTGTGTTTAAATTGTAAAAATTAGATGCC 1740  
ATTAAGAGAAATGAAGGGGAGGATCATCTTAGTGCTTGTTCAGTAGTATTTTAATAT 1800  
CAGCTTCTTGTAACCTTTTCCATGTTGTGAGGGTTGTAAGGGATTGTGTGGCAACAGCAG 1860  
CTTCCCTTGGCTAACTCAATCTTCTACCCATTGCTTAGAGCAGGGAGCCCTCCTTATTTA 1920  
CTACTGAAGACCTTAGAGAACTCCAATTGTTTGGCATATATTTTGGTGGTGGTTTTTAT 1980  
TCCTCCTGGAGAGTTATCTAATTTGTTTCTAAAACAAAACAGCAGCAAAGAAATGAATTA 2040  
AATAC TGGGGTTGAGAATTAAAATTAAGTGATGTTTCAGAGTTGCCCAATATATATGACC 2100  
TGCAAATGATACGAAAAAGTGCAGCATTTAGTGGCAGTTAACAAGAGTGACAAGCCTGGG 2160  
GCAGAGGTACCAAACCTCTCCCACCAGAGAGCTAGAAGTATTTTATACAGTAACTTTGAT 2220  
CTTATGGAAGTGACCTTCAATGCTTATTCTGAAGTAACCTATATGGTGGATACAGGATGA 2280  
ACATTCAGTGCCAGGGAGAATCTTCTCAGGTTGGTTCTCGTTAGAGTGATAAACTGGCTA 2340  
GGGGCCATAGTATTGGTCCTGTTAGGTTTCGGTCATGGAAAAAAAATTTATTTTGGGGTC 2400  
ATCCTGGCTCTAGATGTTATGGGCAAATTTCTGAAACATCTGCAAGAAGGTACCAGTTAA 2460  
TTATAGTGCTTAATATTGGGAATAAGATTAAGCATTATAAATTATAATGTATGGGCCTGTT 2520  
GGTGTAAGCTCAGATAATTAAATAAAAAATAGCATGACTCAAATGAGACATATTCTGCTGA 2580  
ACAGTTTCTACTTCCTCTCCCGCCTGTCCTGTCTATGGGAGACGTGTATAGTTGCTGCTGT 2640  
TTCAGCAAACCACCATAAGACGAAAATGCCTCAGGTTGGGTTGCCAGTCCTTTACAACCTC 2700  
AGCTTGAATTTTACAACAGTGATTGTGAGAATCTGCGTGGTATACACTGAAATATCGGTG 2760  
TGCTGTGATGCAAAGCTTACCTTTGACGATATTGAATGTGATATAGCTGTAGAGAAGTAC 2820  
TTCCTTGCCCTTATGTGAGGATTTCAAACCTATTTTAAATTATGTAGACAAATCAAAGTGGC 2880  
ATTGCTTAATTTTTTAGCAGGCATAATAAGCAAGTTAACAGTAAAAATGCAAAACATGATA 2940  
GCGTTGCTCAATTTTTTAGCAGGTATAATAAGCAGGTTAACAGTAAAAATGCAAAACATGA 3000  
TAGATAAGTCACTTTGAAAATTCAAACCAAAGTTCCTTCACCTTATGGAAATAGGAAATT 3060  
ATGGACTTCAAATTTGGACACTTCCTGTTTACAAAAAGAAATTCAGAGCTAAAAATCATGG 3120  
TAAAAAAAATAGAAACACTTGAGAACTATGGTCTTTATGGGTGCAATTTGAAATCCTTT 3180  
TCATCATCTTACCAGACTAAACTAAGAGCACATACCAAACCTATCTTATGGTTGAAAGTT 3240  
GGGGTTTATTTTTTTATATGAGAATATTATCACTATTACATAACATACTCAGGACAAAGAA 3300  
CTTTGCTCAGGGAACATACCATGTAATATTTTTGTTGTTTCTTTACAGACTAGTCTACAG 3360  
TCCTGCTTACTCAAAACAAACCAAATAAATTATACCTTTATATAAGTATTATGTACTGAT 3420

FIG. 70 (continued from previous page)

GATAGTAACTACCTCTGAGTTTGACACAGATCAAAATTTTTGAATATCAGATATCAGTTA	3480
TCCTATTTTTTATTTTCATGTGAAACTCCTCTAAAGCAGATTCCCTCAACTCTGTGCATAT	3540
GTGAATATCACTGATGTGAACACATTGTTTCATTTACATAGGTAAATATTACTCTGTTTA	3600
CAGCAAAAGGCTACCTCATAGTTGATACATAGCACACCTGTATGTATGCTGTTCCAGCCT	3660
TACAGGTGGCTGATAATTCTCTGGTACAGAACCTTTTTATCTGTATTATAAAATAGCAATT	3720
CACAACTGCATGTTTCTGACAAACACTTGTGAATAATGAAGCATCTCGTTTTAGTTAGCA	3780
AAGTCTCCAAACATTTCCCTTAAATAATCATGTATTTAGTTTAAAGAATTATGGGCACTG	3840
TTCAACTTAAGCAAAACAGAACACGGAAGCAGTCTTAGAAGCACCCTTTGCCCAGAGGT	3900
GGAGGTTGGAAGGGGTAGCAGGGAGAGGGGTTGGTGTATGCAGGTATTCATGCTAGGCAA	3960
AGAGTTTAAAAGACGCCAATGTCCCTTCATTTACTGTCTGTGCTGCCCTGAAGCCAAGCGT	4020
ATTGCAGCATTATAGCCCCAGGCACATAACTAAGTACTGAGCTTGGCTTGGCAAGGAATGAAC	4080
ATGCAATGCCATTACTAGCTATTGAGGGAAAAGGGTCTGTGTGAAGCATCACTTTGCAGG	4140
GATTACTAATGGTGGGGCAGCAGGTCTGTGAATTAAGTTATCTCTTGACCTCACCTCAT	4200
GTCAACACAAAATGTAATTCCTAAACAAGATGCATTGCCAGTCTCTTAGCCCTGTAAAGCTG	4260
ATCTTTTGCTACATGGCAGACTATAATGAAAACATTTTTTATACTTGGGTTTCTAGTCTTC	4320
ACTAGAAGGCCCTTGGATGTATTTTTGCAGTTGAAAGATTTAGAAAAGATTTTTACCTGCTT	4380
ATAACTTGGAAGTTTAGAGTGCAATGTAAGAAAAAGATCAAGAAATGTCATGTTATTAG	4440
CATCAGTCCACCTCCAATATTGCCGATACTTTTTTTATTCTGGCTCAGTTTTATTTTGCA	4500
CCAGTGCGGCCCCAAGTTACTGCTGGTTGTATTTAGTTTGTGAATAGGAGCCCATAAAGTG	4560
TTAATAGACTTTGTAACATTCACATAAGATGAATTATACAGGACATGGGAAATCTCATT	4620
AAGTCTTAAAGTTAATTTAAATTAATTTATCTGTTTTCTCTAAGAAATGTTTATCATAAA	4680
ATATATATGTGTATTTCCCTTTGGTTATAAAATTTGGGAAAGTATGTACAAGTGCAGCT	4740
GCACTGACTTTAATTTTCTAGATGTCTTAATGAGATTTATTTGTTTGTAGAGAAGAACATC	4800
TTGTTAAAGCATCAAACTCTGTCTTACATAGCTGTCAACAGCCTCTTTAAGATGTGGTG	4860
GTTGTATGATCTGTGCTTAATTGTTTCAGTTAGAGTGAGAAGTTGACCTATGATTCATTT	4920
TTAAATTTTATATTTGGAACAAAGCTGCAAGTTATGGTAAAGTACTGTACTGTGAGAAGT	4980
ATTATGATATTTAATGCATCTGTGGCTTAACACTTGTGAGAGTTACCAGCTTGAAAATGA	5040
TGGTGTGACTACCTCTTGAATCACATCTATCAACCACTGGCACCTACCACCAAGCTGGC	5100
TTCAATTAGTATGTGTTGCTTTTTGGTATTAACAATAACCGTACTAGAGACCAAAGTGA	5160
ACCCTGATTTTTTATATGTCCTTAATAATGGTGTTTTTATCTAGTGTTTTTAAATTATCCTG	5220
TGTAGTATTTAGATTACCTCATTGTCCATTTTGACTCATGTTGTTTACAAGTGAAAATAA	5280
AAACACTTGAAGTGTATGTTTTTAAAAGACAAAAAAGGGGTAGATGTTTGAATGCGTTT	5340
CACTCGCATGCAGTCATCTGGAGGGACTGAAGCACTGTTTGCCTTTCTGTACACTCTGGG	5400
TTTTATATTCTCATTTTCATGCCATAATGTCTTATTCTGTCAATTATGGATATGTTGAGGTT	5460
TAAAAAAATTAATTGATTAAAAATAAAACATATAACGTTGGCATTAAAAA	5520
AAAAAAAAAAAAAAAAAAAAA	5542

FIG. 70 (continued from previous page)

AGTAGCTCTAAACCATCTTCACGATTTCTCTTTCTCTCCTCGTGCCCGCCGGAGAGAATAG	60
TTTCGCTGAAAATTTCTCTTTGTCAATGGGATCAGTATTAAATCAGCAATATACAAGTAA	120
AGTATCGCATGCTGTAATGTAAATGTGGCTGAAAAATGGAGTTAAATGAATAAGTACAC	180
GCGGGGCTAGCAAAGGTGGTGGAGAAGAGCCCCGGAAGCTGCCGGAGCCGGCAGAGGAGG	240
AATCCCAGGTTTTGCGCGGAAGTGGCCACTGTAAGTGGTTCAATGTGCGCATGGGATTTG	300
MetGlyPheGly	4
GATTCATCTCCATGATAAACCGAGAGGGAAGCCCCTTGGATATTCCAGTCGATGTATTTG	360
PheIleSerMETIleAsnArgGluGlySerProLeuAspIleProValAspValPheVal	24
TACACCAAAGCAAACCTATTCATGGAAGGATTTAGAAGCCTAAAAGAAGGAGAACCAGTGG	420
HisGlnSerLysLeuPheMETGluGlyPheArgSerLeuLysGluGlyGluProValGlu	44
AATTCACATTTAAAAAATCTTCCAAAGGCCTTGAGTCAATACGGGTAAACAGGACCTGGTG	480
PheThrPheLysLysSerSerLysGlyLeuGluSerIleArgValThrGlyProGlyGly	64
GGAGCCCCTGTTTAGGAAGTGAAAGAAGACCCAAAGGGAAGACACTACAGAAAAGAAAAC	540
SerProCysLeuGlySerGluArgArgProLysGlyLysThrLeuGlnLysArgLysPro	84
CAAAGGGAGATAGATGCTACAACCTGTGGTGGCCTTGATCATCATGCTAAGGAATGTAGTC	600
LysGlyAspArgCysTyrAsnCysGlyGlyLeuAspHisHisAlaLysGluCysSerLeu	104
TACCTCCTCAGCCAAAGAAGTGCCATTACTGTGTCAGAGCATCATGCACATGGTGGCAAAC	660
ProProGlnProLysLysCysHisTyrCysGlnSerIleMETHisMETValAlaAsnCys	124
CCCCACATAAAAAATGTTGCACAGCCACCCGCGAGTTCTCAGGGAAGACAGGAAGCAGAAT	720
ProHisLysAsnValAlaGlnProProAlaSerSerGlnGlyArgGlnGluAlaGluSer	144
CCCAGCCATGCACTTCAACTCTCCCTCGAGAAGTGGGAGGCGGGCATGGCTGTACATCAC	780
GlnProCysThrSerThrLeuProArgGluValGlyGlyGlyHisGlyCysThrSerPro	164
CACCGTTTCCTCAGGAGGCTAGGGCAGAGATCTCAGAACGGTCAGGCAGGTCACCTCAAG	840
ProPheProGlnGluAlaArgAlaGluIleSerGluArgSerGlyArgSerProGlnGlu	184
AAGCTTCCTCCACGAAGTCATCTATAGCACCAGAAGAGCAAAGCAAAAAGGGGCCTTCAG	900
AlaSerSerThrLysSerSerIleAlaProGluGluGlnSerLysLysGlyProSerVal	204
TTCAAAAAAGGAAAAAGACATAACAGGTCTTCTTCATATGTTCTTTCCTTTACCCGGTTG	960
GlnLysArgLysLysThr***	210

FIG. 71

CAAAGTCTACCTCATGCAAGTATAGGGGAACAGTATTTTACAAGCAGTAGCTGACCTGGG	1020
ATTTTAACTACTATTGGGGAACGTGAATTTTTTAAACAGACAAATCACTCTAAGCAAAT	1080
TACATTTGAGCAGGGTGTCATGTTTTATGTTAATTCAGAGAATAAGATACTATGTCTGTC	1140
AATATGTGCATGTGTGAGAGGGAGAGAGCCTGAGTCTGTGTGTGTACATGAGGATTTTTTA	1200
TATAGGAATGTAGACACATATATAAAGAGGCTTTGTCTTTATATATTTGTGTATAGATCA	1260
AAGCACACACCCCTCTCTCATATAATTGGATATTTCCAAGAATTGAAAACCCATGTGAAGC	1320
ATTATAGATAGTTTTAAATTTAACCCTGAGTTTTCTTGAAATACCACTTCTTTTATA	1380
TTATATAAAACTAAAAACGACTGTTACCTTTTGTGTGAACCAAAGGATACTTCAGATC	1440
TCAGAGCTGCCAATTATGGGGTACTAAAGGTTTTTAAGACATCCAGTTCTCCCGAATTTG	1500
GGATTGCCTCTTTTCTTGAAATCTCTGGAGTAGTAATTTTTTCCCCCTTTTTTGAAGG	1560
CAGTACCTTAACTTCATATGCCTCTGACTGCCATAAGCTTTTTTGATTCTGGGATAACAT	1620
AACTCCAGAAAAGACAATGAATGTGTAATTTGGGCCGATATTTCACTGTTTTAAATTCTG	1680
TGTTTTAATTGTAAAAATAGATGCCATTAAGAGAAATGAAGGGGAGGATCATCTTAGTGG	1740
CTTGTTTTCAGTAGTATTTTAATATCAGCTTCTTGTAACCTTTTCCATGTTGTGAGGGTT	1800
GTAAGGGATTGTGTGGCAACAGCAGCTTCCCTTGGCTAACTCAATCTTCTACCCATTGCT	1860
TAGAGCAGGGAGCCCTCCTTATTTACTACTGAAGACCTTAGAGAACTCCAATTGTTTGGC	1920
ATATATTTTTGGTGGTGGTTTTTATTCCTCCTGGAGAGTTATCTAATTTGTTTCTAAAC	1980
AAACAAGCAGCAAAGAAATGAATTAAATACTGGGGTTGAGAATTTAAATTAAGTGGATGT	2040
TCACAGTTGCCCAATATATATGACCTGCAAATGATACGAAAAAGTGCAGCATTTAGTGGC	2100
AGTTAACAAGAGTGACAAGCCTGGGGCAGAGGTACCAAACCTCTCCACCAGAGAGCTAG	2160
AAGTATTTTATACAGTAACTTTGATCTTATGGAAGTGACCTTCAATGCTTATTCTGAAGT	2220
AACCTATATGGTGGATACAGGATGAACATTCAGTGCCAGGGAGAATCTTCTCAGGTTGGT	2280
TCTCGTTAGAGTGATAAACTGGCTAGGGGCCATAGTATTGGTCCTGTTAGGTTTCGGTCA	2340
TGGAAAAAAAATTTATTTTGGGGTCATCCTGGCTCTAGATGTTATGGGCAAATTTCTGAA	2400
ACATCTGCAAGAAGGTACCAGTTAATTATAGTGCTTAATATTGGGAATAAGATTAAGCAT	2460
TATAATTATAATGTATGGGCCTGTTGGTGTAAGCTCAGATAATTAAATAAAAAATAGCATG	2520
ACTCAAATGAGACATATTCTGCTGAACAGTTTCTACTTCTCTCCCGCCTGTCCTGTCAT	2580
GGGAGACGTGTATAGTTGCTGCTGTTTCAGCAAACCACCATAAGACGAAAATGCCTCAGG	2640
TTGGGTTGCCAGTCCTTTACAACCTCAGCTTGAATTTCAACAGTGATTGTGAGAATCTG	2700
CGTGGTATACACTGAAATATCGGTGTGCTGTGATGCAAAGCTTACCTTTGACGATATTGA	2760
ATGTGATATAGCTGTAGAGAAGTACTTCCCTTGCCTTATGTGAGGATTTCAAACCTATTTA	2820
AATTATGTAGACAAATCAAAGTGGCATTGCTTAATTTTTTAGCAGGCATAATAAGCAAGTT	2880
AACAGTAAAATGCAAAACATGATAAGCGTTGCTCAATTTTTTAGCAGGTATAATAAGCAGG	2940
TTAACAGTAAAAATGCAAAACATGATAGATAAGTCACTTTGAAAATTCAAACCAAAGTTC	3000
CTTCACCTTATGGAAATAGGAAATTTATGGACTTCAAAATTGGACACTTCTCTGTTTACAAA	3060
AAGAAATTCAGAGCTAAAATCATGGTAAAAAAAATAGAAACACTTGAGAACTATGGTCT	3120
TTATGGGTGCAATTTGAAATCCTTTTCATCATCTTACCAGACTAAACTAAGAGCACATAC	3180
CAAACCTATCTTATGGTTGAAAGTTGGGGTTTATTTTTTATATGAGAATATTATCACTAT	3240
TACATAACATACTCAGGACAAAGAACTTGTCTCAGGGAACATACCATGTAATATTTTTGT	3300
TGTTTTCTTTACAGACTAGTCTACAGTCCTGCTTACTCAAAACAAACCAAATAACTTATAC	3360
CTTTATATAAGTATTATGTACTGATGATAGTAACTACCTCTGAGTTTGACACAGATCAAA	3420
ATTTTTGAATATCAGATATCAGTTATCCTATTTTTATTTTCATGTGAAAACCTCCTCTAAAG	3480

FIG. 71 (continued from previous page)



CAGATTCCTCAACTCTGTGCATATGTGAATATCACTGATGTGAACACATTGTTTCATTTA	3540
CATAGGTAAAATATTACTCTGTTTACAGCAAAAGGCTACCTCATAGTTGATACATAGCAC	3600
ACCTGTATGTATGCTGTTCCAGCCTTACAGGTGGCTGATAATTCTCTGGTACAGAACCTT	3660
TTTATCTGTATTATAAATAGCAATTACAACTGCATGTTTCTGACAAACACTTGTGAATA	3720
ATGAAGCATCTCGTTTTAGTTAGCAAAGTCTCCAAACATTTCCCTTAAAATAATCATGTAT	3780
TTAGTTTAAAGAATTATGGGCACTGTTCAACTTAAGCAAAACAGAACACGGAAGCAGTCT	3840
TAGAAGCACCACCTTTGCCCAGAGGTGGAGGTTGGAAGGGGTAGCAGGGAGAGGGGTTGGT	3900
GTATGCAGGTATTCATGCTAGGCAAAGAGTTTAAAGACGCCAATGTCCTTCATTTACTG	3960
TCTGTGCTGCCCTGAAGCCAAGCGTATTGCAGCATTATAGCCCCAGGCACATAACTA	4020
AGCACTGGCTTGCCAAGGAATGAACATGCAATGCCATTACTAGCTATTGAGGGAAAAGGG	4080
TCTGTGTGAAGCATCACCTTGCAGGGATTACTAATGGTGGGGCAGCAGGTCTGTGAATTA	4140
AGTTATCTCTTGACCTCACCTCATGTCAACACAAATGTAATTCCTAAACAAGATGCATT	4200
GCCAGTCTCTTAGCCCTGTAAGCTGATCTTTTGTCTACATGGCAGACTATAATGAAAACAT	4260
TTTTATACTTGGGTTTCTAGTCTTCACTAGAAGGCCTTGGATGTATTTTTCAGTTGAAA	4320
GATTTAGAAAGATTTTTACCTGCTTATAACTTGAAGTTTAGAGTGCAATGTAAGAAAAA	4380
AGATCAAGAAATGTCATGTTATTAGCATCAGTCCACCTCCAATATTGCCGATACTTTTTT	4440
TATTCTGGCTCAGTTTTATTTTGCACCAGTGCGGCCCCAAGTTACTGCTGGTTGTATTTA	4500
GTTTGTGAATAGGAGCCCATAAGTGTTAATAGACTTTGTAACATTCACTATAAGATGAAT	4560
TATACAGGACATGGGAAATCTCATTAAGTCTTAAAGTTAATTTAAATTAATTTATCTGTT	4620
TTCTCTAAGAAATGTTTATCATAAAATATATATGTGTATTTCCCCTTTGGTTATAAAAT	4680
TGGGAAAGTATGTACAAGTGCAGCTGCACTGACTTTAATTTTCTAGATGTCTTAATGAGA	4740
TTTATTTGTTTGTAGAGAAGAACATCTTGTTAAAGCATCAAACCTCTGTCTTACATAGCTG	4800
TCAACAGCCTCTTTAAGATGTGGTGGTTGTATGATCTGTGTCTTAATTGTTTCAGTTAGAG	4860
TGAGAAGTTGACCTATGATTCATTTTTTAAATTTTATATTTGGAACAAAGCTGCAAGTTAT	4920
GGTAAAGTACTGTACTGTGAGAAGTATTATGATATTTAATGCATCTGTGGCTTAACACTT	4980
GTGAGAGTTACCAGCTTGAAAATGATGGTGTGACTACCTCTTGAATCACATCTATCAAC	5040
CACTGGCACCTACCACCAAGCTGGCTTCAATTAGTATGTGTTGCTTTTTTGGTATTAACAA	5100
CTAACCGTACTAGAGACCAAAGTGAACCCGTGATTTTTATATGTCTTTAATAATGGTGT	5160
TATCTAGTGTTTTTTAAATTATCCTGTGTAGTATTTAGATTACCTCATTGTCCATTTTGAC	5220
TCATGTTGTTTACAAGTGAAAATAAAAACACTTGAAGTGTATGTTTTTAAAGACAAAAA	5280
AGGGGTAGATGTTTGGAATGCGTTTCACTCGCATGCAGTCATCTGGAGGGACTGAAGCAC	5340
TGTTTGCCTTTCTGTACACTCTGGGTTTTATATTCTCATTTTCATGCCTAATGTCTTATTC	5400
TGTCAATTATGGATATGTTGAGGTTTAAAAAATTAATTGATTAAAAATAAAACATATAA	5460
CGTTGGCATTAAAAA	5507

FIG. 71 (continued from previous page)

Human K#2	1:-----MAEGGASKGGGEEPGKLPAPAEESQVLRGTGHCKWFNVRMG	42
Human	1:-----MGSVSNQQFAGGCAKAAEEAPEEAPDAARAADPQLLHGAGICKWFNVRMG	52
Mouse	1:-----MGSVSNQQFAGGCAKAAEKAPPEAPDAARAADPQLLHGAGICKWFNVRMG	52
Xenopus	1:-----MGSVSNQEITEGLPKSLDGTADIHKSDKSVIFQSGGVCKWFNVRMG	46
Drosophila	1:-----MENVQLENGLERRTTSQSSTSSANPANLASPTTEECGCVRLGKCKWFNVAKG	51
C.elegans	1:MSTVVSEGRNDGNNRYSQDEVEDRLPDVVDNRLTENMRVPSFERLPSPTPRYFGSCKWFNVSKG	65
Human K#2	43:FGFISMINREGSPLDIPVDVFVHQSKLFMEGFRSLKEGEPEVEFTPKK--SSKGLESIRVTGP-GG	105
Human	53:FGFLSMTARAGVALDPPVDVFVHQSKLHMEGFRSLKEGEAVEFTPKK--SAKGLESIRVTGP-GG	115
Mouse	53:FGFLSMTARAGVALDPPVDVFVHQSKLHMEGFRSLKEGEAVEFTPKK--SAKGLESIRVTGP-GG	115
Xenopus	47:FGFLTMTKKEGTDLETPLDVFVHQSKLHMEGFRSLKEGESVEFTPKK--SSKGLESTQVTGP-GG	109
Drosophila	52:WGFLTPN--DGGQ-----EVFVHQSVIQMSGFRSLGEQEEVEFECQR--TSRGLEATRVSSR-HG	107
C.elegans	66:YGFVIDD-----ITGEDLFVHQSNLNMQGFRLDEGERVSYIYIQUERSNGKGREAYAVSVEVEG	124
Cold shock domain(CSD)		
Human K#2	106:SPCLGSERRPKGKTLQKRKPKGDRCYNCGGLD-HHAKECS-LPPQPKKCHYCQSIMHNVANCPHK	167
Human	116:VFCIGSERRPKGKSMQKRRSKGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQSIHNVASCPHK	177
Mouse	116:VFCIGSERRPKGKSMQKRRSKGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQSIHNVASCPHK	177
Xenopus	110:APCIGSERRPKVKGQKRRQRGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQNPNNHMAQCPEK	171
Drosophila	108:GSCQGSTYRPRI---NRRTRRM-RCYNCGEFANHIASECA-LGPQPKRCHRCRGEDHLHADCPHK	166
C.elegans	125:QGLKGSRIHPLG---RKKAVSL-RCFRCGKFATHKAKSCPNVKTDAKVCYTCGSEEHVSSICPER	184
Zinc finger domain		
Human K#2	168:NVAQPPASSQGRQEAESQPCTSTLPREVGGGGCTSPFPQEARAEISERSGRSPQEAASSTKSSI	232
Human	178:AQQGPSAQGKPTYFREEEEEIHSPTLLPEAQN	209
Mouse	178:AQQGPSSQGKPAYF	191
Xenopus	172:AMQAANLEDQPITEEQELIPEIME	195
Drosophila	167:NVTQSHSNSKSISSNNSSSSAAQEKSEET	195
C.elegans	185:RRKHRPEQVAAEEAARMAAEKSSPTTSDDDIREKNSNSSDE	227
Human K#2	233:APEEQSKKGPSVQKRKKT	250

FIG. 72

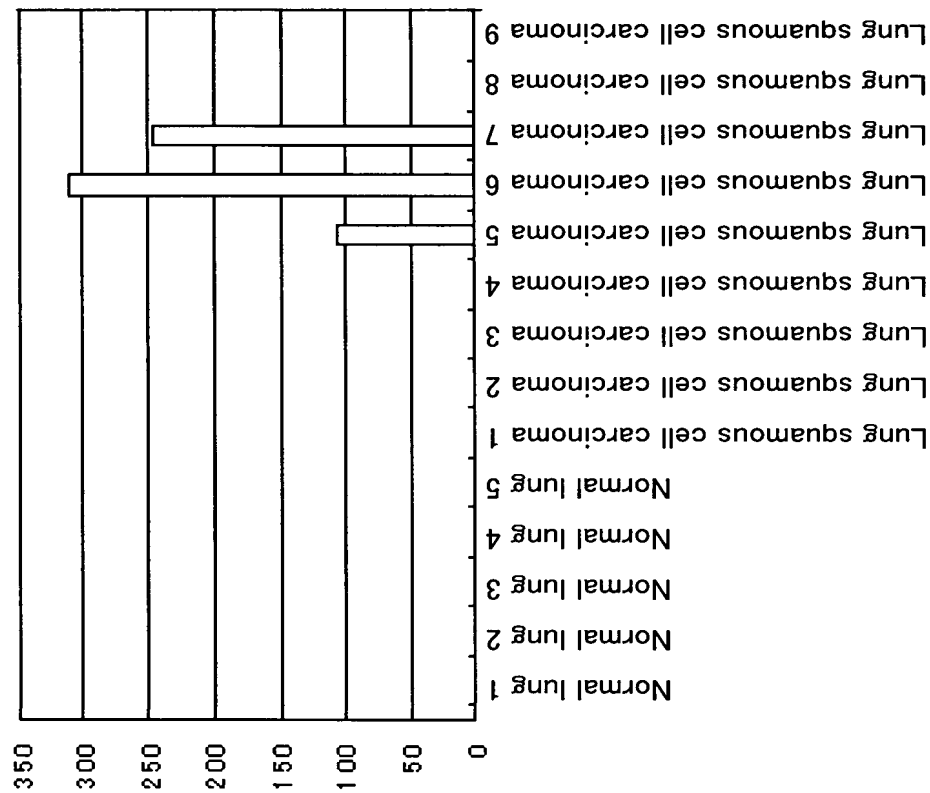


FIG. 73

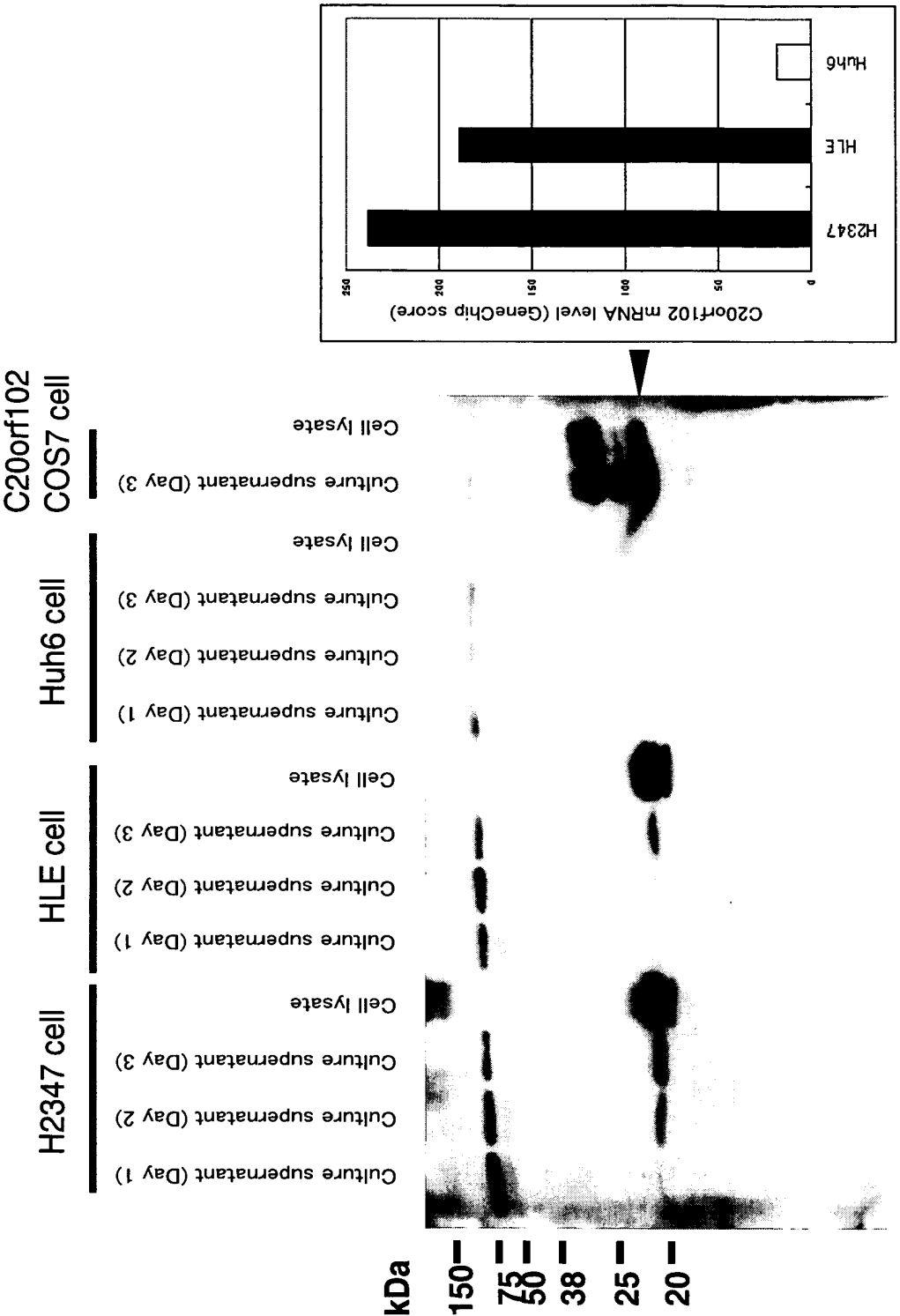


FIG. 74

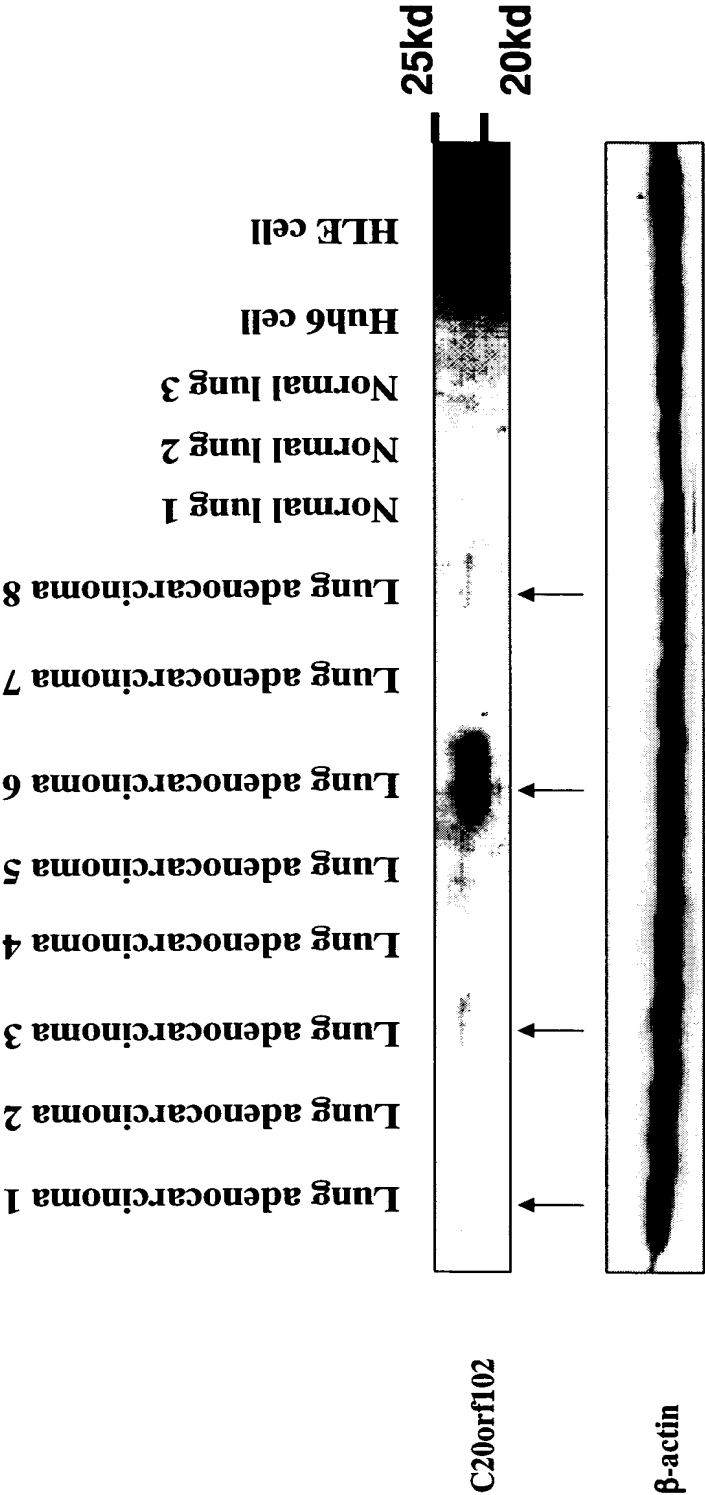
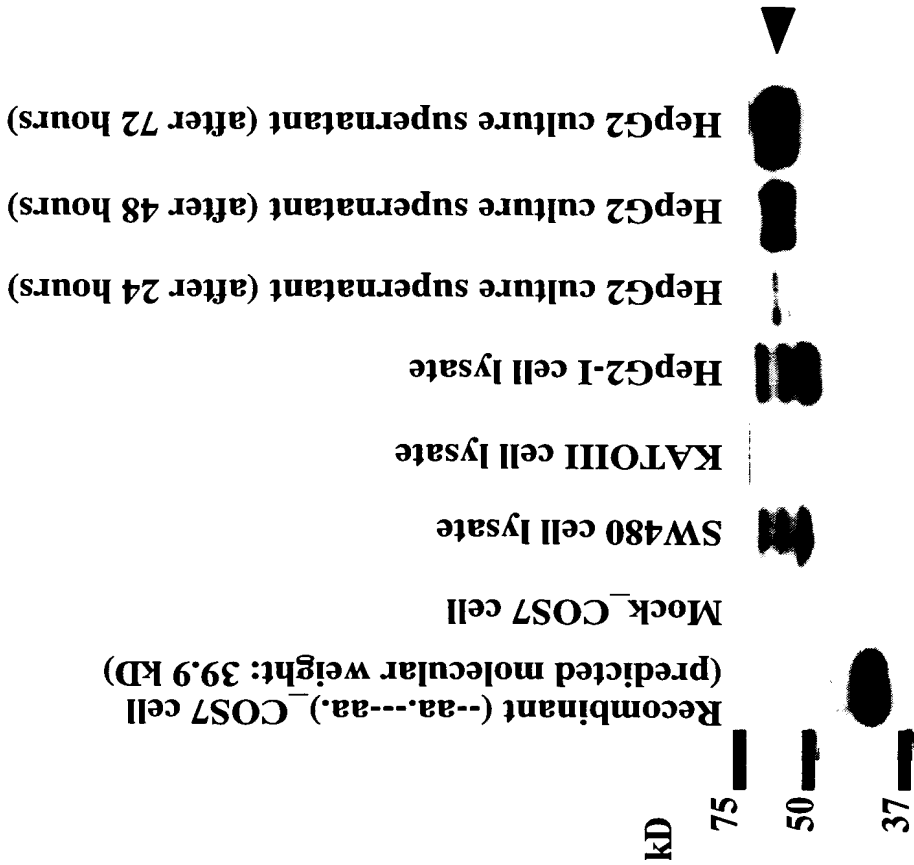
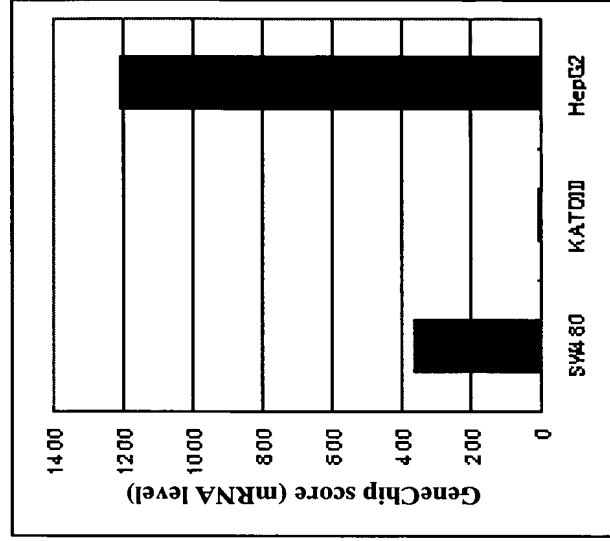


FIG. 75



Predicted molecular weight: 55.7 kDa

FIG. 76



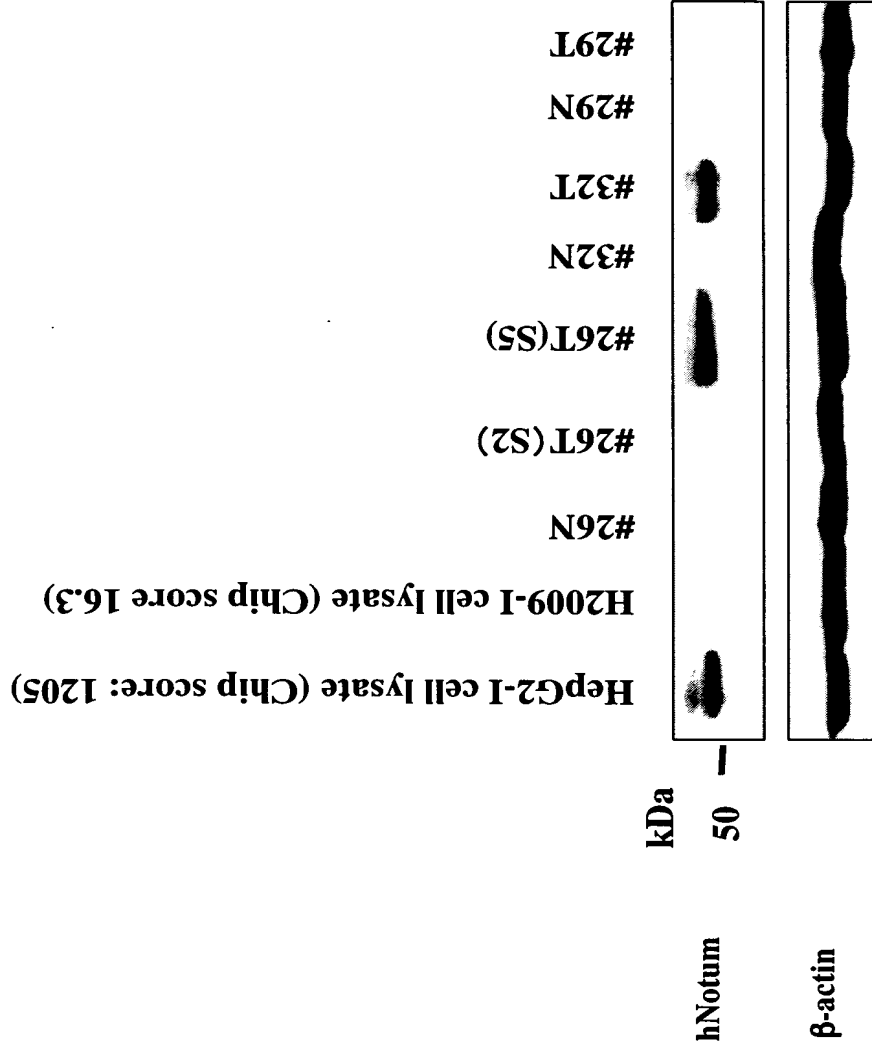


FIG. 77

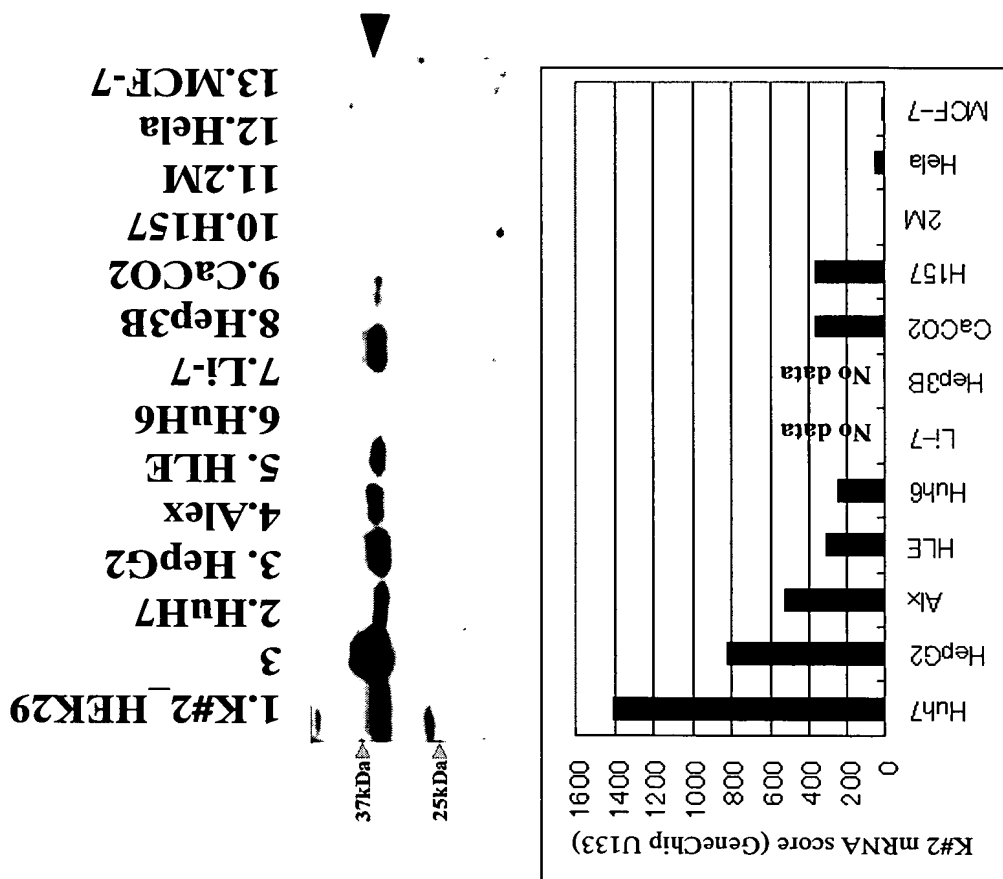


FIG. 78



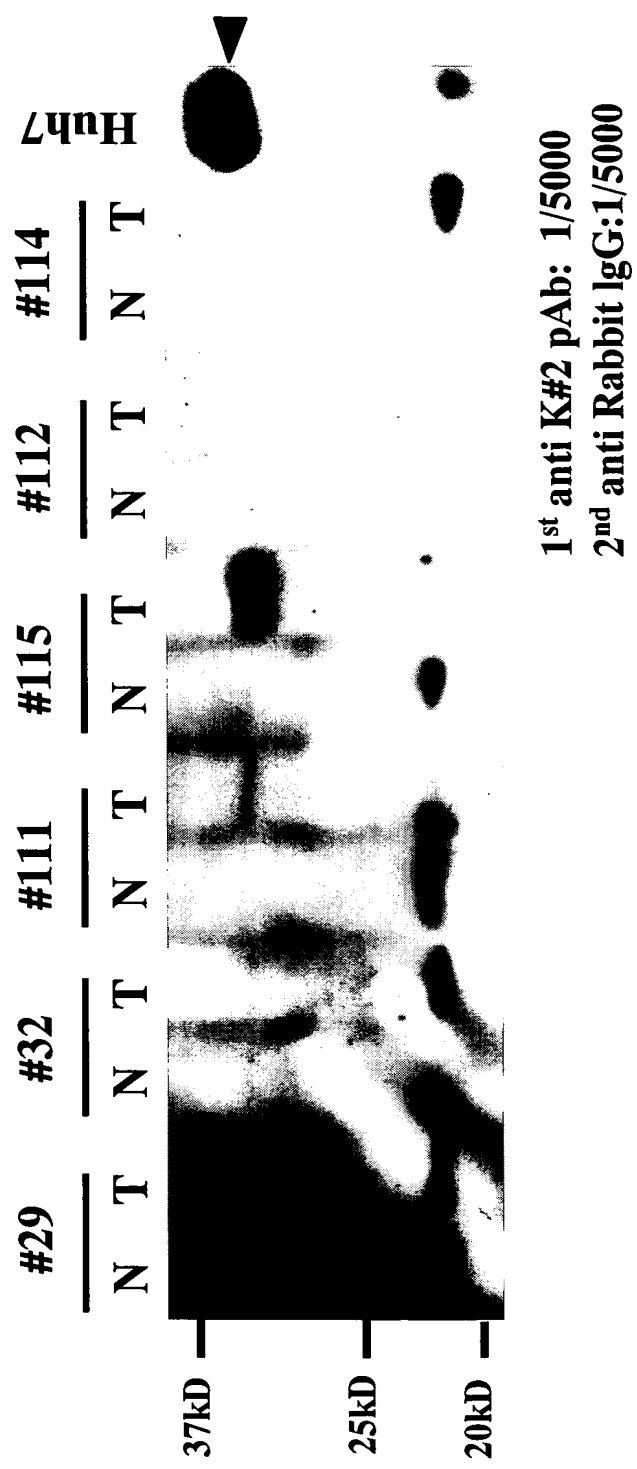
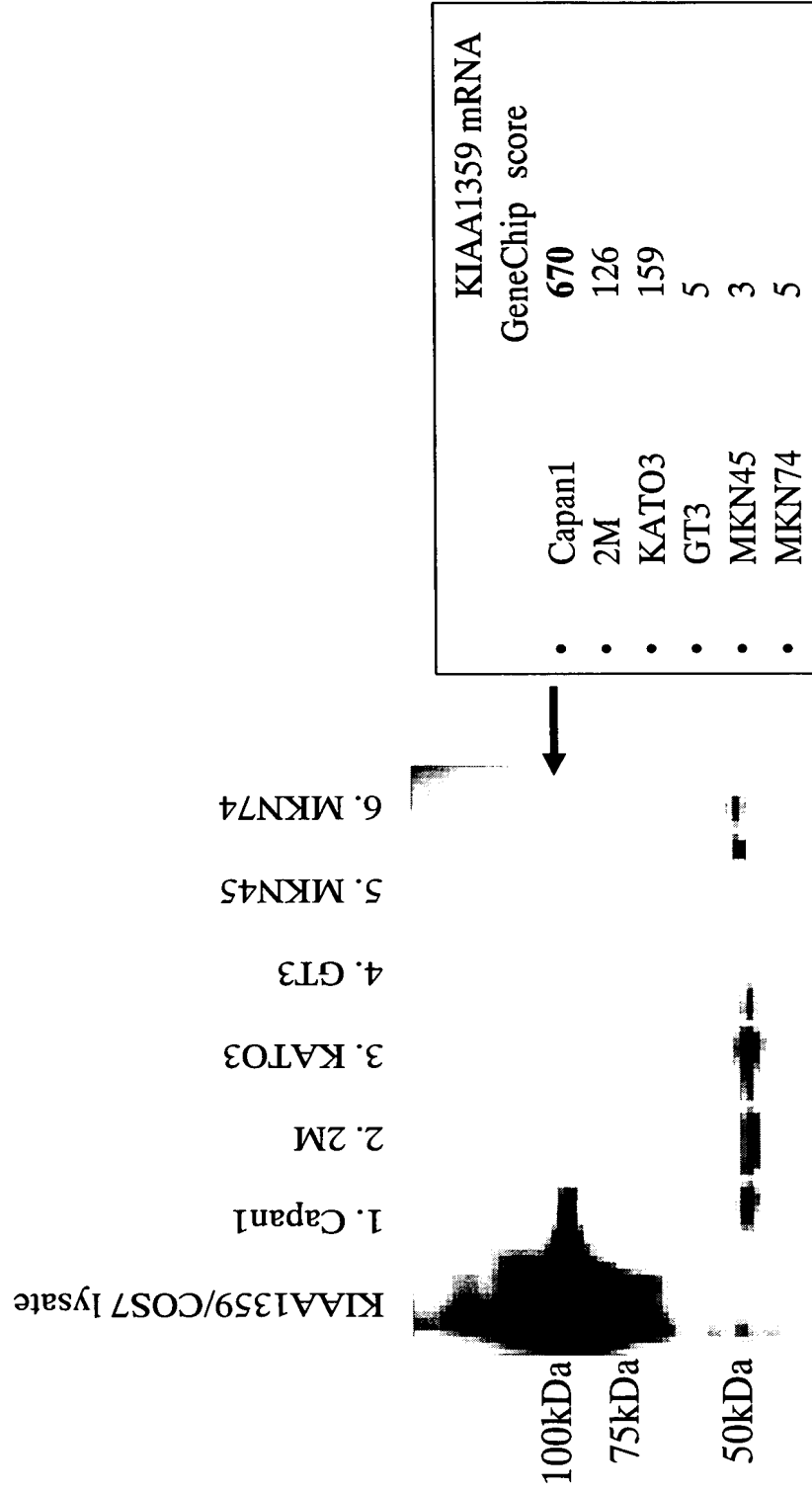


FIG. 79



Evaluation of A8409A

FIG. 80

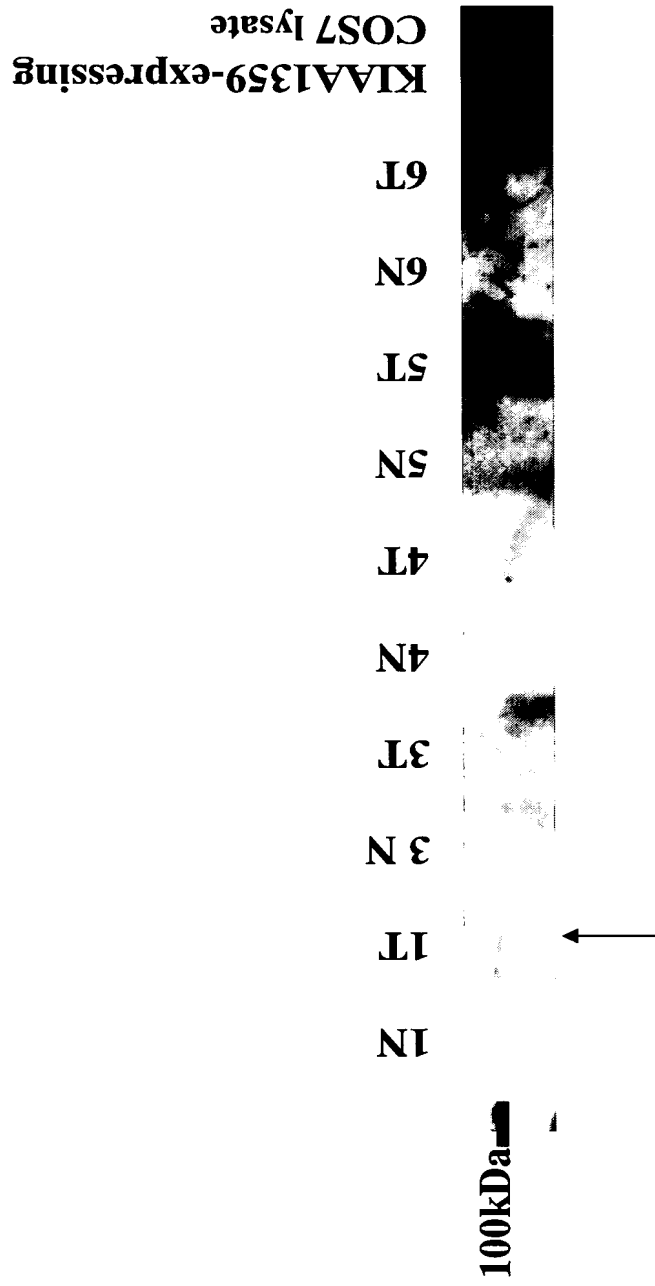


FIG. 81

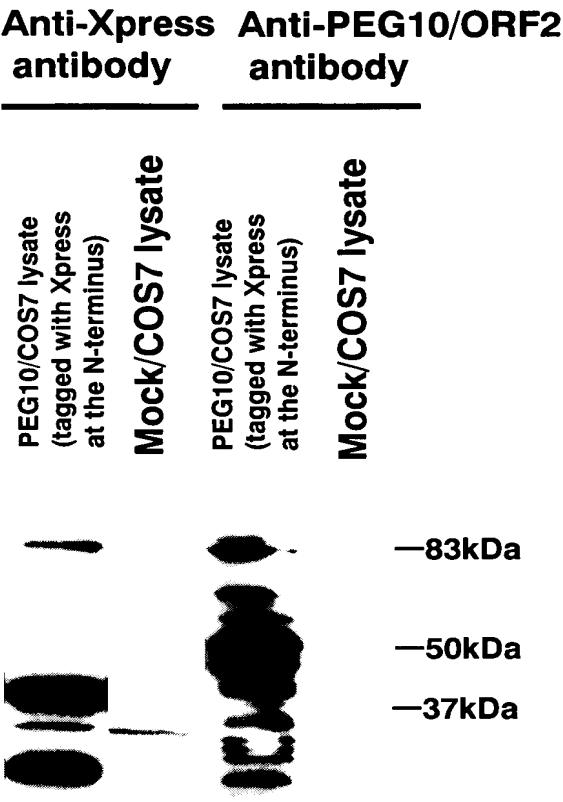


FIG. 82

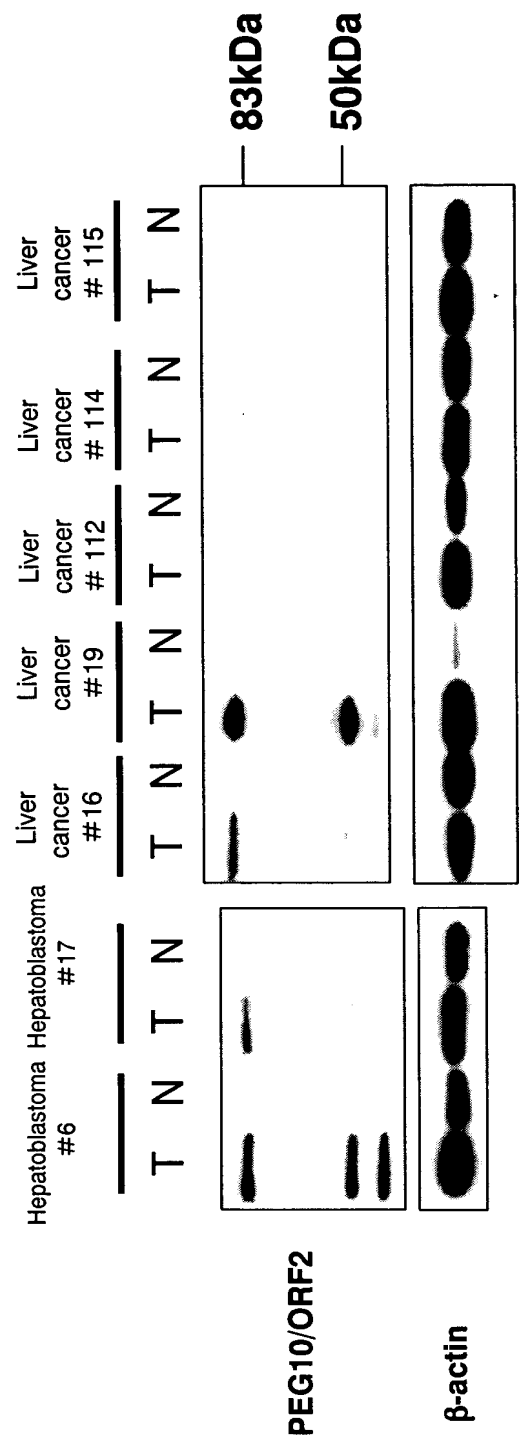


FIG. 83

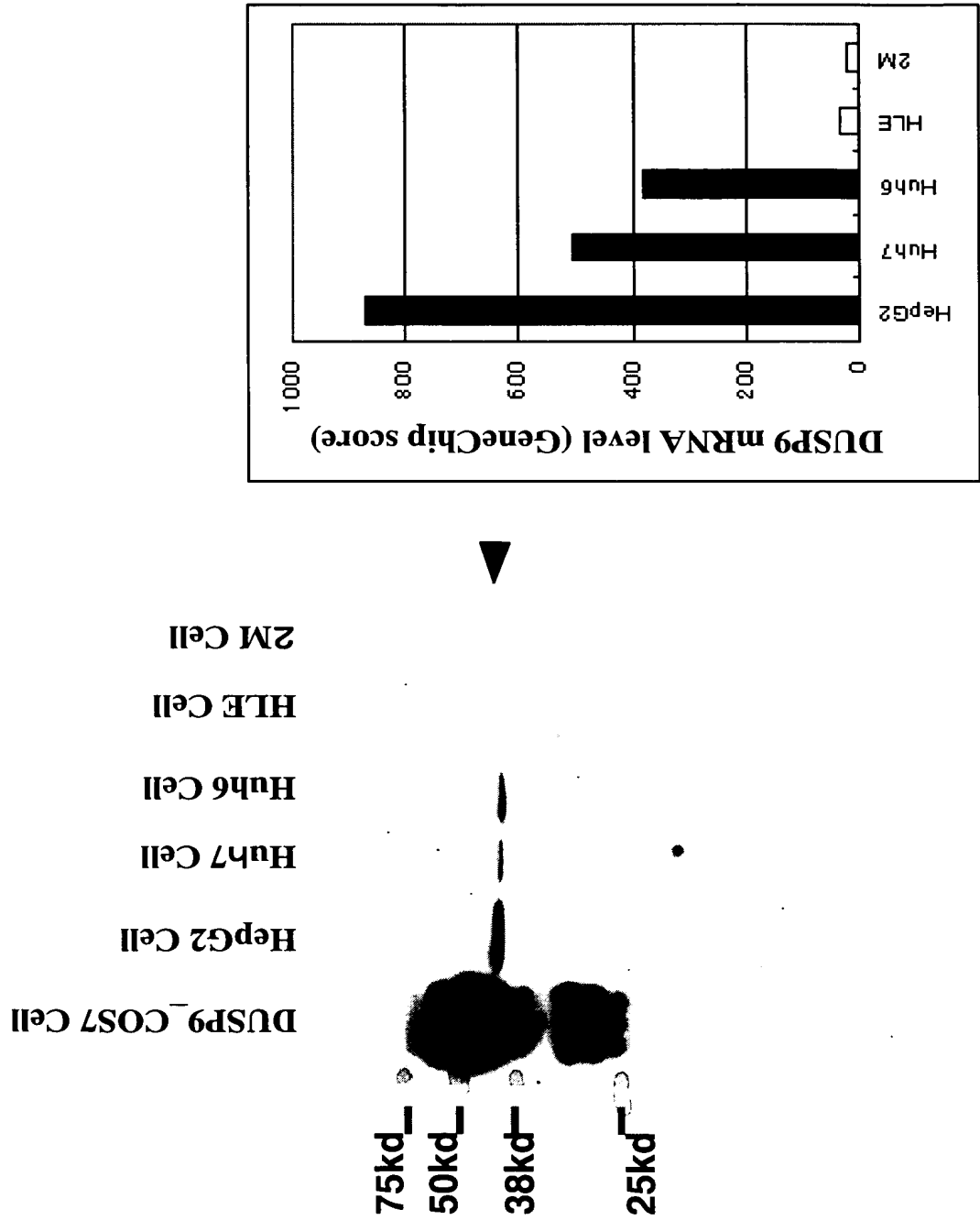


FIG. 84

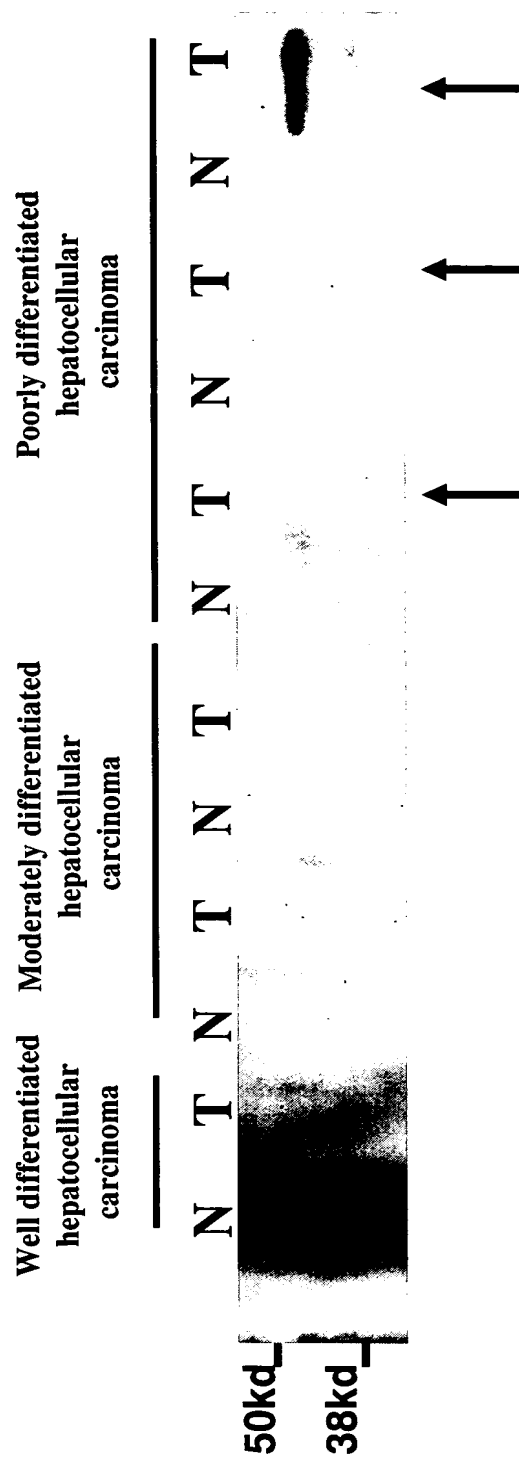


FIG. 85

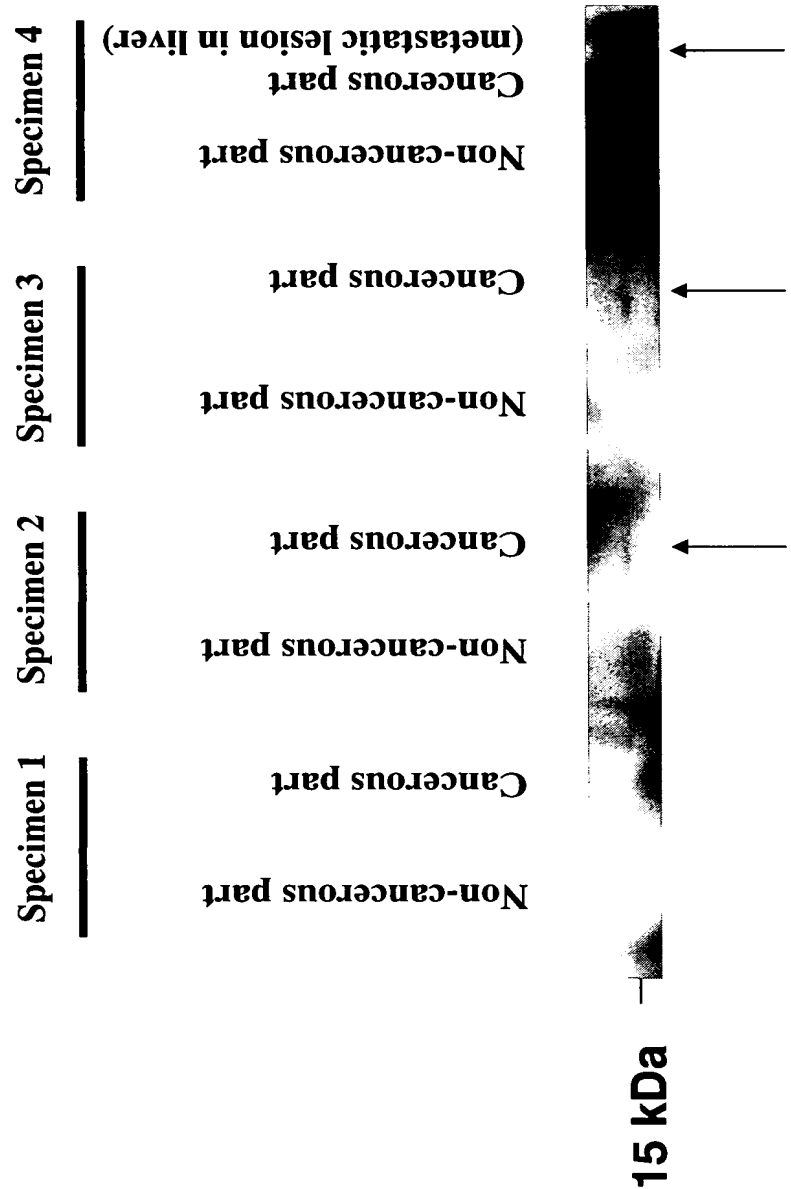


FIG. 86



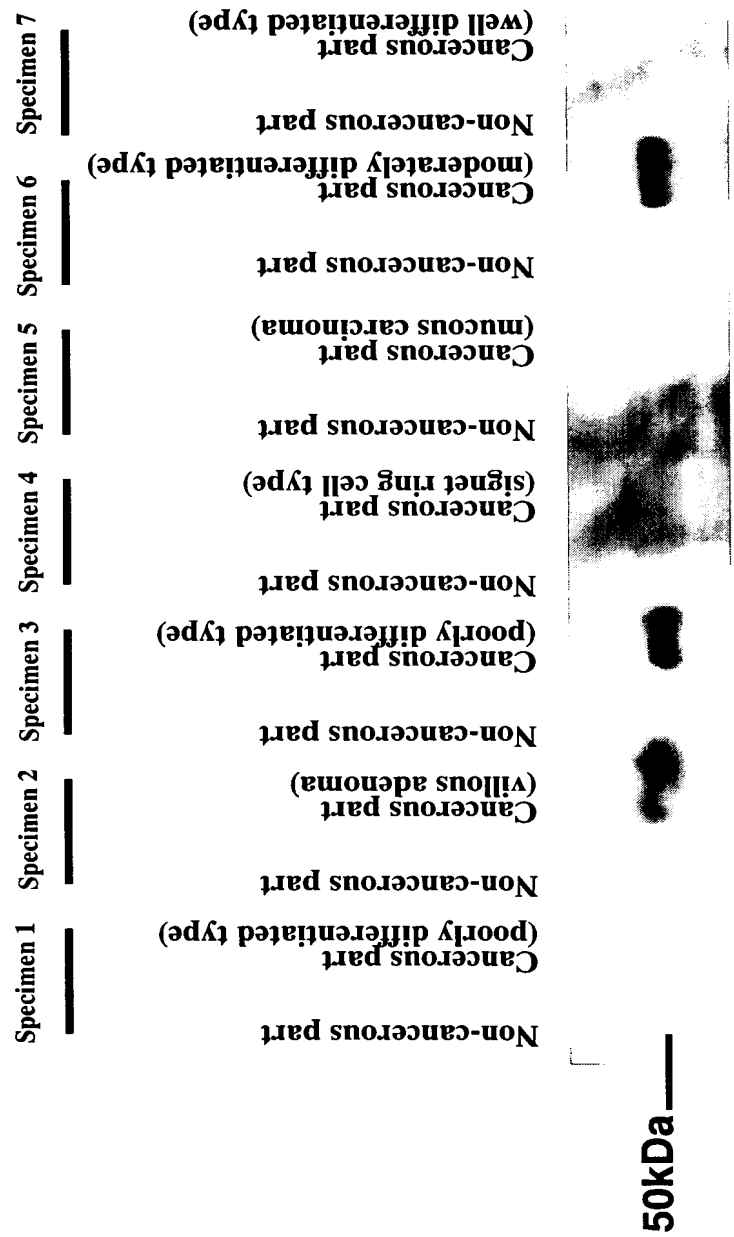


FIG. 87

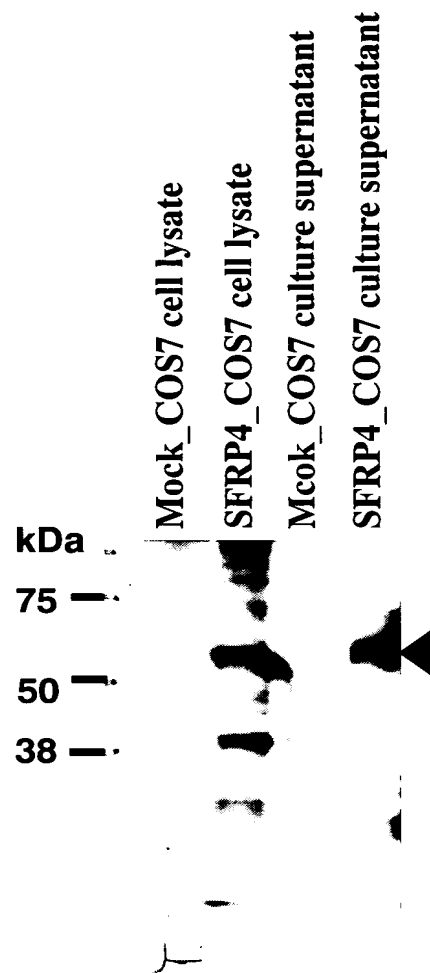


FIG. 88